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October 21, 2004, 11:48:04; Search time 155 Seconds (without alignments) 1053.044 Million cell updates/sec
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2385
1 MSFYSKQDYNMDLELDEYYN.....GFLNNGIKADLVSLIHCLHM 455
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                       2002273 seqs, 358729299 residues
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aar95939 Human YS	7 Human	13	93 Homo E	1 Human	02 Human		9510 Human	3266 Human	4	3016	7604 Human	5230 1	554 Human	52		92 Human	922	Aab85121 Human neu	1110	1860	3320	Aae08004 Human chi	254	Abbs6370 Non-endog
SUMMARIES	QI	AAR95939	AAW29447	AAW29413	AAW37093	AAY57461	AAE08002	ABB84497	ABB79510	AA023266			AAW27604	AAW1523	AAY1455	AAY5257	AAE0795	AAE06692	AAE07922	AAB85121	AAB85110	ABP81860	ADN39350	AAE08004	ABG32254	ABB56370
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AAE02851	AAY52577	AAW37095	AAR95940	AAW29446	AAW29412	AAW37092	AAY57460	ABB84496	AAW27603	AAY14553	AAY52579	AAW15233	AAW15232	ADO29565	AAW27602	AAY14552	AAE08012	AAE08010	AAR95941
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ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

AAR95939 ID AAR	95939	standard; protein; 455 AA.
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X X	AAK95939;	
i i	14-OCT-1996 ((first entry)
DE	Human Y5 receptor	itor.
XX		
×	YS receptor; a	_
ΚW	G protein-coup	agonist; antagonist;
∑	anorexia; tran	ısgenic anımal.
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	01-DEC-1995;	95WO-US015646.
Z Z	02-DEC-1994;	94US-00349025.
AA PA	(SYNA-) SYNAPTIC	TIC PHARM CORP.

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RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
                                      Homo sapiens
                                                                                                           18-NOV-1996;
                                                                                                                                   01-DEC-1995;
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                                                                                                                           Human hippocampal Y5 receptor (AAR95939) was identified as the homologue of rat hypothalamic Y5 receptor (AAR95940), isolated as an 'atypical Y1 receptor'. The receptor balongs to the G protain-coupled receptor superfamily. It is encoded by a cDNA clone (see also AAY30433) that was isolated from a hippocampus cDNA library using rat Y5 receptor cDNA as probe. Recombinant rat Y5 receptor can be produced in prokaryotic or eukaryotic (e.g. COS, 293 or Eff insect) host cells. It is used to identify Y5 ligands (agonists and antegonists) that can be used to treat obesity, bullimia or anorexia, and to raise monoclonal antibodies useful
                                                                     feeding behaviour using Y5 receptor (ant)agonists - increases ses food consumption, for treatment of e.g. obesity or bulimia
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              Weinshank RL;
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            Branchek T,
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                                                                                                          51; Fig 6; 235pp; English
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(first entry)
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           Walker MW,
                                 WPI; 1996-277371/28
                                                                                                                                                                                                                                                                                                   Local Similarity
                                              N-PSDB; AAT30433
                                                                                                                                                                                                                                                                  Sequence 455 AA,
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or decreases
           Gerald CPG,
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26-FEB-1998
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The present sequence represents human hippocampal neuropeptide (NP) Y receptor subtype Y5, with a pharmacological function associated with for example, obssity and eating disorders. The specification relates to a method of treatment and prophylaxis of disorders and diseases associated with with NPY receptor subcype Y5 comprising administering to a warm-blooded animal, including man, in need of such treatment a warm-herapeutically effective amount of a quinazolin-2,4-disazirine compound. These disorders and diseases include e.g. eating disorders, obseity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss, sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage, shock, congestive heart failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to correct PI field.)
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epileptic seizure, migraine; sleep disturbance, prophylaxis; eating disorder; quinazolin-2,4-diazirine.
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Tintelnotblomley M, Schilling W, Criscione
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61 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120

VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120

61

121

241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYS 300

KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360

301

241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300

181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS

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RESULT 4
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361 RVKRSVTRIKKRSRSVFYRLTILLLVFAVSMMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of new and known hetero:aryl compounds as NPY Y5-receptor antagonists - for treating and preventing eating disorders, diabetes, dyslipidaemia, hypertension, memory loss, epilepsy, migraine, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents human hippocampal neuropeptide (NP) Y receptor subtype Y5, with a pharmacological function associated with for example, obesity and eating disorders. The specification relates to a method of treatment and prophylaxis of disorders and diseases associated with with NPY receptor subtype Y5 comprising administering to a warm-blooded animal, including man, in need of such treatment a therapeutically effective amount of a new heteroaryl compound. These disorders and diseases include e.g. eating disorders, obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, depression, anxiety, cerebral haemorrhage, shock, congestive heart failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                               Human hippocampal neuropeptide Y Y5 receptor, NPY Y5; prophylaxis, bullmia nervosa; diabetes; dyslipidaemia; hypertension; memory loss; epileptic siezure; migraine; aleep disturbance; pain; depression; sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea; congestive heart failure; eating disorder; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2385; DB 2; Length 455; 100.0%; Pred. No. 1.2e-236; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n T, Rigollier P, Yamaguchi Y, Schilling W, Criscione L;
                                                421 HILGMMSCCINPILYGFLNNGIKADLVSLIHCLHM 455
                                                                              HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                                                                                                                                                                                                                  Human hippocampal neuropeptide Y Y5 receptor.
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                                                                                                                                                              AAW29413 standard; protein; 455
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(first entry)
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Best Local Similarity 100.0
Matches 455; Conservative
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24-FEB-1998
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361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSMMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
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301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPENSDVHEL 360
                                                361 RVKRSVTRIKKRSRSVFYRLTILILLVPAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIÇ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding canine hypothalamic atypical neuro:peptide Y/peptide Yyreceptor, YS - useful for identification of compounds which are capable of modifying feeding behaviour.
                                                                                                                                                                                                                                                                                                                                                                                                         Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity; feeding behaviour; modification; atypical neuropeptide.
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                                                                                                                         421 HILGMMSCCINPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                                                                               421 HILIGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
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97US-00803600.
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N-PSDB; AAV00622.
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1 MSFYSKQDYNWDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF 1 MSFYSKODYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF

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Nucleic acid encoding a human neuropeptide Y receptor useful in genetic

WPI; 1999-590415/50. N-PSDB; AAZ39046.

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identified by administering a potential antagonist to a transgenic mammal as above, and determining whether the substance alleviates the physical and behavioural abnormalities displayed by the transgenic mammal as a result of overactivity of a Y5-R. Agonists can be identified in a similar manner, but where the abnormality is alleviated by increasing the activity of Y5-R
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                                                                                                                    Gaps
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Pred. No. 1.2e-236;
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                                                                                     The present sequence represents the human hippocampal Y5 receptor. The Y5 teceptor is a G-protein coupled neuropeptide Y receptor found throughout the mammalian nervous system and is a powerful stimulant of feeding behaviour. Cells expressing DNA encoding the Y5 receptor can be used to determine whether a ligand specifically binds to a Y5 receptor. These cells or a cell extract, is exposed to the ligand and then any binding between the ligand and the receptor can be detected. The cells can also be used to determine whether a ligand is a Y5 receptor can also agonist. The binding of chemical compounds to a Y5 receptor can also determined and whether they activate or inhibit the activation of the Y5 receptor can also be determined using cells expressing the receptor. The antagonists can also be detected with these cells
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100.0%; Pred. No. 1.2e-236;
ive 0; Mismatches 0;
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                                          Disclosure, Fig 6, 87pp, English
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engineering
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Huntington's disorder; Parkinson's disorder; eating disorder; seizure; locomotor; anxiety disorder; limbic seizure; tranquilliser; human.
                                                                                                                                          "Second intracellular loop domain"
                                                                                                                                                                       'note= "Second extracellular loop domain'
                                                                                                                                                                                                                                                      439. .455
/note= "C-terminal intracellular domain"
                                                                        72. .84
/note= "First intracellular loop domain"
                                                                                                            /note= "First extracellular loop domain"
126. 146
                                                                                                                                                                                    242. .378
/noce= "Third intracellular loop domain"
379. .401
                                                                                                                                                                                                                                 "Third extracellular loop domain"
                                                  "N-terminal extracellular domain
                                                                                                                                                                                                                                         115. .438
/note= "Seventh TM domain'
                                                                                      B5. .105
/note= "Second TM domain"
106. .125
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/note= "Second intracell:
168. .188
/note= "Fourth TM domain"
                                                                                                                                                                                                          379. .401
/note= "Sixth TM domain"
                                                          51. .71
/note= "First TM domain"
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                                                                                                                                                                             221. .241
/note= "Fifth TM domain"
                                    Location/Qualifiers
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/note= "T'
415.
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WO200155103-A2

02-AUG-2001

29-JAN-2001; 2001WO-US002804

28-JAN-2000; 2000US-0178652P.

(NEUR-) NEUROGEN CORP

Krause J; Brodbeck R, Bennett M,

WPI; 2001-514543/56. N-PSDB; AAD14734.

New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development.

Example 2; Page 55-56; 72pp; English.

The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmebrane proteins with seven membrane proteins with seven membrane spanning transmembrane. (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, highlow blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug atlons, and as basis for drug disorvery and development. The NPYS receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is human NPYS receptor

Sequence 455 AA,

Length 455; Score 2385; DB 4; Pred. No. 1.2e-236; 100.0%; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                        HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300
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                                                  1 MSFYSKODYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
                                                                                VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG
Gaps
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Indels
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95US-00566096.
98US-00200673.
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Conservative
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N-PSDB; AAF88821.
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01-DEC-1995;
25-NOV-1998;
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Matches 455;
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This invention describes a novel method of modifying feeding behaviour of a subject which involves administering to the subject an amount of a compound which is a Ys receptor agonist or antagonist effective to increase or decrease, respectively, the consumption of food by the subject so as to modify feeding behaviour of the subject. The product of the invention has metabolic, anorectic, antidepressant, tranquiliser, antidigratine, analgesto, hypotensive, creabroprotective, cardiant, antidigratine, analgesto, hypotensive, creabroprotective, cardiant, antidigratine, analgesto, anorectic antidipressant, tranquiliser, antidigration and haemostatic activity and can be used in a vaccine. Ys receptor agonist or antagonist compounds are useful for treating an abnormality alleviated by the inhibition or activation of Ys receptor, in a subject. Antibodies raised against the receptor are useful for treating an abnormality alleviated by the inhibition or activation of Ys receptor, in a subject. Antibodies raised against the receptor are useful for treating an appormality in a subject, where the abnormality includes anioraxia, sexual/reproductive disorder, depercation, anxiety, memory loss, migraine, pain, epileptic sizulure, hypertension, anxiety, memory loss, migraine, pain, epileptic failure, sleeve disturbance, nasal congestion, and diarrhoea. This secures of the inventing in the stream of the invention of the invention
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Modifying feeding behavior of subject, useful in treating feeding disorders, involves administering to subject Y5 receptor agonist or antagonist, to increase or decrease consumption of food by subject.
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                                                                                                         Claim 53; Fig 6; 102pp; English.
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nes 455; Conservative
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The present sequence is the protein sequence for the human neuropeptide (S (NPYS) receptor. In an example from the invention, chimeric receptors including human NPS receptor sequences were constructed, and used to assay the binding activity of compounds of the invention. Substituted spiro(isobenzofuran-1,4'-piperidin) 3-ones and 3H-spiroisobenzofuran-1,4'-piperidines capable of modulating NPS receptor activity are provided. Such compounds may be used to modulate ligand binding to NPS receptors in vivo or in viro, and are particularly useful in the treatment of a variety of disorders, eg. eating disorders such as obesity or bulimia, psychiatric disorders, diabetes and cardiovascular disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VSLLGFWGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWRFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or 3H-spiroisobenzofuran-1,4'-piperidine, useful for treating, e.g. eating disorder, psychiatric, cardiovascular disorder or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
                                                                                          antiinflammatory; nootropic; neuroprotective; cardiovascular; hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiant; carebroprotective; antidepressant; haemostatic; tranquillizer; neuroleptic; analgesic; antianginal; nephrotropic; uropathic; gastrointestinal; antianginal; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Darrow JW;
X, Elliott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2385; DB 5;
100.0%; Pred. No. 1.2e-236;
ive 0; Mismatches 0;
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Tran J, Zheng
                                                                           Y5; NPY; NPY5; receptor; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 675; Page 129-130; 134pp; English.
                                   Human neuropeptide Y5 receptor.
                                                                                                                                                                                                                                                                                                                  11-DEC-2001; 2001WO-US047863
                                                                                                                                                                                                                                                                                                                                                      12-DEC-2000; 2000US-0254990P
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De Lombaert S, Hutchison A,
(first entry)
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Best Local Similarity 100.
Matches 455, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-547845/58.
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                                                                                                                                                                                                                                         WO200248152-A2
                                                                         Neuropeptide
23-SEP-2002
                                                                                                                                                                                                         sapiens
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Gaps

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Indels

Length 455;

180 180 240 300

HISVCRSISCGLSNKENRLEENEMINLTLHPSKKKGGPQVKLSGSHKWSYSFIKKHRRRYS 300

HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYS

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421

ABB79510 ABB79510

RESULT 8 ABB79510

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Gaps . 0

Indels

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Mismatches

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455; Conservative

Matches

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420
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                                                           361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360
               301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL
                                                                                                           421 HILIGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                            421 HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                                                                                                                                                                                    Human neuropeptide Y5 receptor (NPY5) protein.
                                                                                                                                                                              AAO23266 standard; protein; 455 AA
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                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  EP1306085-A1
                                                                                                                                                                                                                             25-SEP-2003
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                                                                                                                                                                                                     AA023266;
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This invention relates to novel ligands (derivatives of 2-cyclohexyl-4-phenyl-1H-imidazole) for the neuropeptide V5 (RPV5) receptor. The NPV5 receptor mediates a variety of physiological effects and is involved in appetite regulation, hormone release and blood pressure. Ligands that modulate the NPV5 receptor inhibit or enhance NPV binding such that they can be used to treat a variety of conditions including feeding disorders (obestry and bulinia), psychiatric disorders, diabetes and cardiovascular diseases such as hypertension. Further uses relate to to the treatment of cerebral infarction, epilepsy, sofhizophrenia, despession, angina, sudden cardiac death, vasospasm, arkhythmia, urinary incontinence, Crohn's disease and asthma. As such these ligands can be described variously as enerolaging, animimaliammatory, mootropic, vasotropic, anticonvulsant and uropathic. This polypeptide sequence is the human neuropeptide YS (NPYS)
New 2-cyclohexyl-4-phenyl-1H-imidazole derivatives are modulators of neuropeptide Y5 receptor activity, useful for treating e.g. eating or psychiatric disorders.
                                                                                                                                                                                                                                                   Example 10; Page 39-41; 63pp; English.
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Zheng X;

De Lombaert S,

Brielmann HL,

Blum CA,

2003-543553/52.

N-PSDB; AALS6583

Score 2385; DB 6; Length 455; Pred. No. 1.2e-236;

100.0%; 100.0%;

Query Match Best Local Similarity

Sequence 455 AA;

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                       1 MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
                                                                                                                                                                                                                                                                  CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
                                                                             61 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG
                                                                                                       61 VSLLGFWGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG
                                                                                                                                                                                                                                        181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
1 MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
                                                                                                                                                           KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PRIM-) PRIMAL INC
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Li F; Zeng H;

JE, Gragerov A, Hohmann J, Pavlova MN, Vassilatis D,

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to compound the sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention, methods of screening for associated with GPCRs of the invention, methods of screening for compounds useful in the treatment of GPCR related diseases, at transgenic compounds useful in the treatment of GPCR related diseases, at transgenic compounds useful in the treatment of GPCR related diseases, at transgenic mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived comprising a mice; kits comprising several mice, ach of which has a mutation in a different GPCR gene of the invention; and kits comprising comprising a which hybridise to GPCR polymocleotides of the invention. The invention further discloses variants of the GPCR polymocleotides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of discasses including neurological disorders (e.g., Alzhaimer's disease, deprending on trintable bowel closuscens of the adrenal gland; disorders of the colon or intestines; grandome); cardiovascular disorders (e.g., autoimmune disorders (e.g., and macmia or leukaemia); immune disorders; (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., osteoarthritis, protein disorders (f.the kidney, liver, lung, breast, ovary, obseity, protein teleficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breaset obseity, and officency-related diseases or vitamin Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina Claim 151; SEQ ID NO 666; 542pp; English. electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. pectoris, Parkinson's disease. Gaitanaris GA, Bergmann JE, Madisen L, Mcilwain KL, Pa WPI; 2004-390329/36. N-PSDB; ADO30001.

Sequence 455 AA;

ò 300 120 180 240 240 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYS 300 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360 9 9 241 HTSVCRSISCELSNKENRLEENEWINLTLHPSKKSCPQVKLSGSHKWSYSFIKKHRRRYS MSPYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF MSFYSKODYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS Gaps .. 0 100.0%; Score 2385; DB 8; Length 455; 100.0%; Pred. No. 1.2e-236; ive 0; Mismatches 0; Indels 0; 3est Local Similarity 100.
Matches 455; Conservative н 61 121 181 Query Match g dd qq ò δ ò d ò 엄 ઠે

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1 MSFYSKODYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF 1 MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF

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The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and control of limbic seizures. The present sequence is african green monkey (AGM) NPYS receptor ö receptor proteins comprising a single polypeptide chain of useful as targets for drug actions, and as basis for drug Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein; transmembrane; TM domain; therapy; obesity; blood pressure; eiplepsy; thuntington's disorder; Parkinson's disorder; eating disorder; seizure; locomotor; anxiety disorder; limbic seizure; tranquilliser; 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC .. 0 Length 455; African green monkey (AGM) neuropeptide Y5 (NPY5) receptor. Indels HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455 HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455 99.5%; Score 2373; DB 4; 99.3%; Pred. No. 2.1e-235; ive 2; Mismatches 1; Example 2; Page 70-72; 72pp; English. AAE08016 standard; protein; 455 AA Krause J; New chimeric receptor proteins 29-JAN-2001; 2001WO-US002804. 28-JAN-2000; 2000US-0178652P. (first entry) discovery and development. african green monkey; AGM Best Local Similarity 99.3 Matches 452; Conservative Bennett M, Brodbeck R, Cercopithecus aethiops. (NEUR --) NEUROGEN CORP. WPI; 2001-514543/56. N-PSDB; AAD14746. Sequence 455 AA; WO200155103-A2. 01-NOV-2001 02-AUG-2001. amino acids, AAE08016; 301 361 421 421 Query Match AAE0801 D. g ઠે à

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A novel human receptor for the neurotransmitters neuropeptide Y (NPY) and peptide YY (PYY) is designated NPY YS receptor. Its amino acid sequence was deduced from a human genomic DNA clone (see AAT87940). Rat NPY YS has also been identified (see AAW27602.03). These polypeptides can be expressed in host (e.g. human 293) cells. The effects of NPY include blood pressure regulation, memory enhancement, anxiolysis/sedation and increased food intake. The receptor can therefore be used to screen for
                                                                                                                                                                                                           KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360
                                                                                                                                                                                                                                                               RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
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                                                                                                                                                                                                                            KKTACVLPAPERPSGENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360
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                                                                                                                                                         HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
                   KVMCHIMPFLQCVSVLVSTLILSIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
                                                                                                      CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
                                                                                                                     CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG
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                                                   KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide Y receptor Y5; NPY Y5; peptide YY; NPY/YY receptor; neurotransmitter; antagonist; agonist; obesity; anorexia; hyperlipidaemia; diabetes; gene therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecule encoding neuro:peptide Y receptor - useful identify antagonists and agonists, e.g. treat obesity, diabetes, hyperlipidaemia and anorexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neuropeptide Y receptor (NPY Y5)
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antagonists and agonists capable of controlling these conditions; antagonists could be used to treat obesity and diabetes by reducing appetite and food consumption, while agonists could be used to treat
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                                                                                                                                                                        Length 445;
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This sequence represents the human neuropeptide Y5 receptor (Y5) protein. The protein is useful for screening for compounds able to be used as agonists and antagonists to the Y5 receptor, especially for the treatment obesity and diabetes and for developing antibodies for the detection of
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                                                                                                                                                            A novel human neuropeptide Y (NPY)-Y1-like receptor (AAM15230), designated NPY-Y5 receptor, is a G-protein coupled receptor of NPY, which is involved in appetite-obesity regulation. Its amino acid sequence was deduced from isolated genomic (AAT66909) and foetal brain cDNA (AAT66910) sequences. Rat (AAM12232) and mouse (AAM12233) NPY-Y5 receptors have also been identified. NPY-Y5 receptors can be expressed on the cell surface of host (pref. CHO, human embryonic kidney 293 or insect Sf9) cells. The receptors or host cells can be used to screen for NPY (ant)agonists useful as potential hypotensives, cardiovascular drugs, neuronal growth factors, anti-psychotic, anti-obesity or anti-diabetic drugs
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                                       DNA encoding the neuro:peptide Y-Y5 receptor - for screening for NPY-Y5 antagonists and agonists, useful as anti-obesity agents, anti-hypertensive agents cardiovascular drugs, etc.
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N-PSDB; AAT66909, AAT66910
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Gaps

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Length 445;

70 9 130 120 190 180 250 240 310 300 370 360 430 420

Human NPY (neuropeptide Y) Y5 receptor.

28-FEB-2000

Homo sapiens

Human

AAY14554 XX AC AAY: XX AX DT 31-i XX XX XX XX KW Hum KW Obe XX XX XX

RESULT 14

XX XW New Central KW C

Neuropeptide Y; NPY; receptor; Y5; G-protein coupled; expression; chimeric; pharmacological property; pertipheral nervous system; central nervous system; physiological; activity; food intake; feeding; thermogenesis; blood pressure; hormone release; gut motility; smooth muscle tone; sleep; circadian rhythm; neuronal excitability; nociception; mood; emotional response; seizure activity; diuresis; natrivesis; calciuresis; antisense; agonist; antagonist; obesity; hypertension; epilepsy; sexual dysfunction; jet lag.

Homo sapiens.

US5985616-A.

16-NOV-1999".

07-JAN-1998; 98US-00003199.

07-JAN-1998; 98US-00003199

(SCHE) SCHERING CORP.

Parker EM, Rudinski MS, Strader CD;

WPI; 2000-012792/01. N-PSDB; AAZ46232. Chimeric mammalian neuropeptide Y5 receptor polypeptides useful for treating a range of disorders including jet lag, hypertension and sexual disfunction.

Example; Col 37-40; 24pp; English.

This sequence represents human neuropeptide Y (NPY) Y5 receptor, CDNA encoding which was isolated and amplified from a human neuroblastoma cell line using primers A24615-24623. The receptor was transiently expressed in COSI calls, but its level of expression was found to be significantly lower in comparison to that of the rat NPY Y5 receptor (AAY52579). The invention relates to a chimeric rat/human NPY receptor, comprising the 5' untranslated region (5' UTR) and extreme 5' coding region (105 bp) of the rat Y5 receptor CDNA, appended to mucleotides 365-commeric construct yielded levels of expression higher than the name y5 receptor. The pharmacological properties of the chimeric cative rat Y5 receptor. The pharmacological properties of the chimeric receptor were similar to these of the naive human Y5 receptor. NPY is widely distributed in both the peripheral and central nervous systems and cative thermogenesis, blood pressure, hormone release, gut motility, smooth muscle tone, sleep and circadian rhythms, neuronal excitability, conciception, mood and emotional responses. NPY mediates these concipied receptors (designated Y1-Y6): The Y5 receptor mediates concident coupled receptors (designated Y1-Y6): The Y5 receptor mediates concident coupled receptors (designated Y1-Y6): The Y5 receptor mediates concident coupled receptors (designated Y1-Y6): The Y5 receptor mediates concident coupled receptors (designated Y1-Y6): The Y5 receptor mediates concident acceptor, associated mucleic acids (e.g., expression excitability and seizure activity, diuresis, natriuresis and calciuresis. The chimeric Y5 receptor, associated mucleic acids (e.g., expression excitability and calculars such as abosity, hypertension, epilepsy, sexual dysfunction and citates and associated with abnormal expression/activity of NPY

Sequence 445 AA;

Query Match

97.7%; Score 2330; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 5.5e-231;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0

11 MDLELDEYNKTLATENNTAATRNSPFYWDDYKSSVDDLOYFUSLGEFMGNL 70

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a y

241 GLSNKENRLEBENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAP 300 ERPSQENHSRILDENFGSVRSQLSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK 370 430 250 OCVSVIVSTLILISIALVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 190 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPEVCLTVSHTSVCRSISC 301 ERPSQENHSRILPENFGSVRSQLSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC GLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYSKKTACVLPAP 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL KRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 421 NPILYGFLNNGIKADLVSLIHCLHM 445 431 NPILYGFLNNGIKADLVSLIHCLHM 455 181 251 311 191 g ò g à qq à g ò

Search completed: October 21, 2004, 12:09:59 Job time : 156 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 21, 2004, 11:59:55 ; Search time 40 Seconds (without alignments) 1094.466 Million cell updates/sec Run on:

US-09-771-956-13 2385 1 MSFYSKQDYNMDLELDEYXN......GFLNNGIKADLVSLIHCLHM 455 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

No. Score Match Length DB ID No. Score Match Length DB ID 1 481.5 20.2 366 2 871152 4 80 20.1 382 2 845390 6 464.5 19.2 3.6 2 871852 7 480 20.1 382 2 845133 8 480 20.1 382 2 845133 9 455.5 19.4 375 2 83388 10 404 16.9 375 2 83388 11 384 16.9 370 1 152315 12 377 15.8 436 2 0.75599 13 377 15.8 436 2 0.75599 14 368.5 19.4 2 A42885 15 367 15.4 449 2 A41738 16 386.5 14.9 430 2 171898 17 15.4 449 2 A41738 18 351.5 14.7 447 2 A4730 18 351.5 14.7 447 2 A4730 19 384 2 32817 10 600 600 600 600 600 600 600 600 600 6			eko'			SUMMARIES	
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	53	0	2	ω	ď	627	al prot

neurokinin 2 recep	hypothetical prote	glucocorticoid-ind	hypothetical prote	galanin receptor 1	protein AC7.1 [imp	hypothetical prote	probable allatosta	gastrin-releasing	hypothetical prote	neurokinin 2 recep	tachykinin recepto	dopamine receptor-	neurokinin 2 recep	neurokinin 3 recep	neurokinin 3 recep
JQ1059	T22076	D40470	T19340	159336	B88684	T32714	JC7319	A41007	T19186	800516	S17783	D56849	157957	A34916	J01517
н	7	0	7	N	~	~	0	~	~	,⊣	~	~	~	N	Н
398	412	443	374	349	390	391	357	384	376	384	519	514	384	452	465
	7:3	12.6	12.4	12.3	12.3	12.3	12.1	12.1	11.9	11.9	11.9	11.8	11.8	11.8	11.8
12.7	H	٠.													
		300	295.5	294	293.5	293	288.5	288.5	285	285	284	282.5	281.5	280.5	280.5

ALIGNMENTS

RESULT 1	
neuropep C;Specie C;Date:	neuropeptide Y/peptide YY receptor Y1 - African clawed frog C,Species: Xenopus laevis (African clawed frog) C,bate: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R; Marten	R.Martens, G.J.; Blomgvist, A.G.; Roubos, E.W.; Larhammar, D. suhmitted to the RMR. Data Library, November 1993
A, Descri A, Refere	Appearingtion: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenor A/Reference number: 871152
A; Access A; Molecu A: Residu	A;Accession: S71152 Molecule type: mRNA A:Residnes: 1-366 <mar></mar>
A; Cross-	references: UNIPROT: P34992; EMBL: L25416; NID: 9409169; FIDN: AAA49918.1; PID: 94091
A;Experi R;Blomgv	A;Experimental source: brain, hypothalumus R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.
Biochim. A;Title:	Biophys. Acta 1261, 439-441, 1995 Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA fi
A;Refere	ince number: S55924; MUID:95260870; PMID:7742373
A, Status	A:Status: preliminary; nucleic acid sequence not shown
A;Molecu A;Residu	A;Molecule type: mRNA A;Residues: 1-278,'T',280-366 <blo></blo>
A; Cross-C; Superf C; Keywor	A,cross-references: EMBL:125416; NID:9409169 S.Supertamily: neuroxinin I receptor C.Keywords: G protein-coupled receptor; transmembrane protein
Ouerv Match	Match 20.2%: Score 481.5: DB 2: Length 366:
Best Loo Matches	Similarity 26.4%; Pred. No. 6e-31; 4; Conservative 75; Mismatches 128; Indels
δλ	OYKSSVDDLQYFLIGL-YTFVSLLGFMGNLI
QQ	6 YFBNLSVPNNISGNITFPISEDCALPLPMIFTLALAYGAVILLGLSGNLALIIIL 61
Š	VVLFCSPFTLTSVLLDOWNFC
ф	62 KQKEMRNVTNILIVWLSFSDLATIMCLPFTLIVTLMDHWIFGEVMCKLNBY1QCVSVTV 121
δλ	Ĕ.
qq	122 SIFSLVLIAIERHQLIINPRGWRPNNRHACFGITVIWGFAMACSTPLMMYSVLTDEPF 179
ò	SWPSDSYRIAFTIE
qa	180 KNISLDSYIGKYVCLEDFPEDKFRLSYTTLLFILGYLGFLCFIFVCYTKI 229
٥٠	255 KENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAPERPS 314
qq	230 236
ζŏ	315 QENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIKKRSR 374

Db 62 IIIILKQKEMRNYTNILIVNLSFSDLVAIMCLPFTFVYTLMDHWVFGBAMCKLNPFVQC 121	QY 133 VSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVE 192	QY 193 LQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSIS 249	Oy 250 CSJSNORMELENDRINILITHERKKSGEQUKLEGSSHWARSERIKKHRRKSKKTACVLPA 109 235	
: ::	OY 375 SVPYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVVCICHLLGMMSCCLNPIL 434 SPECIAL STREET STREE	OY 435 YGFLNNGIKADL 446 Db 315 YGFLNKNFQRDL 326	AMERIUF 2 AMERICA STRUCTURE OF STRUCTURE OF THE NUMBER OF THE NUMBER OF STRUCTURE	

A;Status: preliminary A;Molecule type: DNS A;Rolecule type: DNS A;Residues: 1-375 <res 1="" a;cross-references:="" c;superfemily:="" embl:u35232;="" neurokinin="" nid:g1063629;="" pid:g106="" pidn:aac50280.1;="" receptor<="" th="" uniprot:ps0391;=""><th> : : 218 LLLFQYCLPLGFILVCYARIYRRLQRQGRVF 285 HKWSYSFIKKHRRYSKKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVP</th></res>	: : 218 LLLFQYCLPLGFILVCYARIYRRLQRQGRVF 285 HKWSYSFIKKHRRYSKKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVP
Query Match	DD 249 HKGIYSLKAGHWKQ
iminarity 25.1%; Conservative	Db 263
Qy 49 DLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAPSDILVVLFCSPFT 108	OY 405 DNLISNRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADLVSLI 450 Db 292 HEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALV 337
109 LTSVLLDQWMPCKVMCHIMPPLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYP	RESULT 8
99 AVYIIMDYWIFGETLCKWSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYL 158	S63685 neuropeptide Y receptor D type - mouse
OY 169 LIATVWTLGFAICSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTIS 224	13-Mar-1997 #text_change 09-Jul-2004
OY 225 LLLVQYILPLVCLTVSHTSVCRSISCGLSNKENRLEENEMINLTIHPSKKSGPQVKLSGS 284	Ridregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J. FEBS Lett. 381, 58-62, 1996 A/Itle: Cloning and characterization of a novel receptor to pancreatic polypeptide, a mel
S HKWSYSFIKKHRRYSKKTACVLPAPERPSOENHSRILPENFGSVRSQLSSSSKFIPGVP 344	1
Db 249 HKGTYSLRAGHMKQ 262	
ILVFAVSWMPLHLFHVVTDFN 404	A;cross_references: UNIPROT.Q61041; EMBL:U40189; NID:91223969; PIDN:AAC52442.1; PID:91223; C;Superfamily: neurokinin 1 receptor
263VNVVLVVMVVAFALMLPLHVFNSLED	19.2%; Score 458; DB 2; Length 375; ilarity 25.1%; Pred. No. 4.7e-29;
405 DNLISNRHFKLVYCICHLIGMMSCCLNPILYGFLNNGIKADLVSLI, 45	Matches 105
DD 292 HEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALV 337	QY 49 DLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFT 108
RESULT 7	100 THORITALITICIESTES THE CONTROL OF THE CONTROL O
pancreatic polypeptide receptor - human C:Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text change 09-Jul-2004	QY 109 LISVLLDQWMFGK.MCH.MPFLQCVSVLVSTLLISIALVKYHMIKHPISNNLIANHGYF 168
K.; Brenner, S.; Co	QY 169 LIATVWTLGFAICSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSY 217
L Data Library, December 1995 401018	
A.Accession: G02300 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA	Qy 218 RIAFIISLLLVQYILPLVCLTVSHTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGP 277 Db 211 RIYTTFLLLFQYCIPLAFILVYTRIYGR 241
A:Residues: 1-375 <yan> A:Cross-references: UNIPROT:P50391; EMBL:U42387; NID:g1314327; PIDN:AAB07759.1; PID:g131 C;Superfamily: neurokinin 1 receptor</yan>	Oy 278 QVKLSGSHKWSYSFIKKHRRYSKKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSS 337
Query Match 19.4%; Score 463.5; DB 2; Length 375;	Db 242 260
ocal Similarity 25.1%; Pred. No. 1.7e-29; s 102; Conservative 72; Mismatches 121;	QY 338 KPIPGVPICFEIKPEENSDVHELRVKRSVTRIKKRSRSVFYRLTILILVPAVSWMPLHLF 397 Db. 261
QY 49 DLQYPLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNPLIGNLAFSDILVVLFCSPFT 108	398 HVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNDILYGPLNNGIKADLVSLIHC 45
QY 109 LTSVLLDQWMFGKVMCHIMPFLQCUSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYF 168	Db 285 NTLEDWYQEAIPACHGNLIFLWCHLLAMASTCVNPFIYGFLNINFKKDIKALVLTCHC 342
Db 99 SVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYL 158	RESULT 9 139187
QY 169 LIATUWTLGFAICSPLPVFHSLVBLQETFGSALLSSRXLCVESWPSDSYRIAFTIS 224 Db 159 GIVIWVIAQUASLPF-LANSILENVFHQHSKEFLADKVVCTESWPLAHRTIYTTF 217	neuropeptide Y/peptide YY receptor Y2 - human N;Albernate names: neuropeptide Y/peptide YY receptor type 2 C.Species: Homo saniens (man)
	C;Date: 01-Mar-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004 C;Accession: I39187; I39163; G02301

receptor cloned from

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A;Molecule type: mRNA
XResidues: 1-584 KKUB-
A;Cross-references: UNIRROT:07M3J6; GB:AX128640
C;Comment: This receptor, the first functionally active orphan Drosophila sulfakinin G-p:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sulfakinin receptor protein, DSK-R1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Unn-2002 #sequence_revision 03-Unn-2002 #text_change 09-Uul-2004
C;Accession: JC7809
B;Cchem. Biochem. Biophys. Res. Commun. 291, 313-320, 2002
A;Title: Cloning and functional expression of the first Drosophila melanogaster su A;Reference number: JC7809; PMID:11846406; MUID:21835488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIKKRSRSVFYR 379
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                                                                                                      1920 protein-coupled receptor UHR-1 - rat
G protein-coupled receptor UHR-1 - rat
G proteins: Rattus sp. (rat)
C paces: Rattus sp. (rat)
C pacesion: 15215
R Welch, S. K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A.Title: Sequence and tissue distribution of a candidate G-coupled receptor A, Reference number: 152315; MUID:95251659; PMID:7733930
A.Accession: 152315
A.MID:95251659; PMID:7733930
A.Status: preliminary; translated from GB/EMBL/DDBJ
A, Seatus: 1370 ex RES
A, Residues: 1370 ex RES
A, Cossidues: GB.S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528
C, Superfamily: neurokinin 1 receptor
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16.9%; Score 404; DB 1; Length 370;
Best Local Similarity 25.8%; Pred. No. 9.8e-25;
Matches 111; Conservative 66; Mismatches 138; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --HDVRLCEEFWGSQERQRYYAMGLLGTYLLPLAILLSYVRV--
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A.Title: Expression cloning and pharmacological characterization of a human hippocampal A; The electrone number: 139187; WIID:96070760; PMID:7592910

A, Accession: 139187

A, Accession: 139187

A, Residues in 1-31, 20261-22664

A, Feridues in 1-31, 20261-22664

A, Fraitie: Coloning and functional expression of a cDAR encoding a human type 2 neuropeptid A; Recence number: 1139163; MID:96032678; PMID:559383

A, Accession: 13163

A, Accession: 13163

A, Midecule type: many

A, Molecule type: many

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19.1%; Score 455.5; DB 2; Length 381;
Best Local Similarity 25.4%; Pred. No. 7.7e-29;
Matches 104; Conservative 72; Mismatches 114; Indels 119;
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23.5ep-1997 #sequence_revision 23.5ep-1997 #text_change 09-Jul-2004
C;Accession: JC5599
R;Lacourse, K.A.; Lay, J.M.; Swanberg, L.J.; Jenkins, C.; Samuelson, L.C.
Biochem. Biophys. Res. Commun. 236, 630-635, 1997
A;Title: Molecular structure of the mouse CCK-A receptor gene.
A;Reference number: JC5599; MUID:97395148; PMID:9245702
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                    ; Score 384; DB 2; Length 584;
; Pred. No. 6.8e-23;
81; Mismatches 186; Indels 100;
                                                      ie region #status predicted <TVR1>
ie region #status predicted <TVR2>
ie region #status predicted <TVR3>
ie region #status predicted <TVR3>
ie region #status predicted <TVR4>
ie region #status predicted <TVR5>
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                   A;Map Dosition: 17
F;115-139/Domain: transmembrane re;
F;149-167/Domain: transmembrane re;
F;189-207/Domain: transmembrane re;
F;259-250/Domain: transmembrane re;
F;253-30/Domain: transmembrane re;
F;41-494/Domain: transmembrane re;
F;467-491/Domain: transmembrane re;
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A)Cross-references: UNIPROT:008786
A)Note: translation not complete
                                                                                                                                                                                                                                                                                                    16.1%;
24.5%;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.5%
Matches 119; Conservative
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A,Gene: dsk-rl
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C;Species: Oryccolagus cuniculus (Gomestic rabbit)
C;Species: Oryccolagus cuniculus (Gomestic rabbit)
C;Accession: S50150
R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
Biochim. Biophys. Acta 1219, 321-327, 1994
A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.
A;Reference number: S50150
A;Accession: S50150
                                                                                                                                                                                                      LGLENETLFCLDQPQPS-KEWQSAVQIL-----LYSFIFLLSVLGNTLVITVLIRNKRM
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                                                                                                                                     LATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQ
                                                                                                                                                                                                                                                                                                      83 KTIVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 LLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISCGLSNKENRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIFGSALCKITTYLMGTSVSVSTLNLVAISLERYGAICKPLOSRVWQTKSHALKVIAATW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 VCLTVSHTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKK
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                                                  Gaps
                                                  70;
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    ed. No. 1.7e-22;
Mismatches 175;
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.larity 25.7%; Pred. No. 2.5e-22;
Conservative 73; Mismatches 155;
    Pred. No.
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                                              84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 YCFMNKRFRLGFMATFPC 395
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C;Superfamily: neurokinin 1 receptor
                                         109; Conservative
    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 IVMMVAY---
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Best Local Simi
Matches 104;
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Best Local R
Matches 109
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295 HRR-----RYSKKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFE 348

TANHGYPLIATUWTLGPAICSPLPVFHSLVELQETT 	LLPSDAM LTLHPSKKSGP	ON 320 RILPENRGAURSAGESSERFIGOUPTCERKEENSOVHELAVKESVTRIKKEERSUVFN 379 239 GLOSGOSCHLARERS
DD 252 ERKASTGSGRFEDNDGCYLQR-SKPTRQLELQQLSGGGGRVSRIHSS 298 QY 349 IKPEENSDVHELRVKRSVTRIKKRSRSVFYRLTILLILVFAVSWMPLHLFHVVTDFNDNL1 408 DD 299SSAAAMAKKRVIRMLMVIVVLFFLCWMPIFSANAMRAYDIVSA 342	Qy 409 SNRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADLVSLIHC 452	RASHIT 14 AA269. AA269. Conception member of the convey rate Conception member of the convey rate Concession. AA268. AA269. AA260. AA260. AA260. AA260. AA2

TTDFNDNLISNRHFKLVYCICHL	318 VIVFTCCWLPFNILQLLLNDEEFAHWDPLPYVWFAFHWLAMSHCCYNPIIXCY 370	438 LINNGIKADLVSLIH 451	371 MWARFRSGFVQLMH 384	
ò	Ор	8	QO	

292 -------MLTV 317

QQ

Search completed: October 21, 2004, 12:14:03 Job time: 42 secs

Fri Oct 22 09:43:52 2004

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 21, 2004, 11:57:55; Search time 192 Seconds (without alignments) 1363.518 Million cell updates/sec Run on:

US-09-771-956-13 2385 1 MSFYSKQDYNMDLELDEYYN.....GFLNNGIKADLVSLIHCLHM 455 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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NY2R CHICK Q9YHX1 O97505	NY4R_HUMAN Q6FH06	NY4R_RAT OS74 <u>6</u> 3	OCHA00	AAN 28939 Q6Y6A6	AA062563	NY2R_MOUSE	NY4R_MOUSE
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385 374 375	375	375	375	371	371	385	375
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473.5 471 466	464.5	464	462	462 459	459	458.5	458
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ALIGNMENTS

RESULT 1

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AAH42416 PRELIMINARY;
AAH42416;
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02-MAR-2004 (TEMBLEE]. 27,
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Best Local Similarity 100.0
Matches 445, Conservative
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                                                                                                                                                                        EMBL; U56079; AAC50623.1; -

BMBL; U66275; AAC50623.1; -

BMBL; U94320; AAC50623.1; -

BMBL; U94320; AAC50623.1; -

BMBL; AY322538; AAC5195.1; -

BMBL; AY322538; AAC5195.1; -

BMM; 602001; -

BMM; 602001; -

CO; GO:0004983; F:neuropeptide Y receptor activity; TAS.

GO; GO:000786; P:G-protein coupled receptor protein signalin. .; TAS.

GO; GO:000786; P:G-protein coupled receptor protein signalin. .; TAS.

InterPro; IPR00021; GPR00409.

InterPro; IPR00033; NPYS receptor.

InterPro; IPR00031; NPYS receptor.

InterPro; IPR00031; NPYS receptor.

INTERPRO; IPR00011; NPY receptor.

INTERPRO; IPR0017; TAS.

RECEPTOR RECEPTOR RECEPTION: TASE NEG.

PROSITE; PS50262; GPROTEIN RECEPTION: Clycoprotein; Palmitate;

ROSPORTE; PS50262; GPROTEIN RECEPTION: Clycoprotein; Palmitate;

ROSPORTE; PS50262; GPROTEIN RECEPTION: TASE NEG.

ROSPORTEIN RECEPTOR CLYCOPROTEIN RECEPTION CLYCOPROTEIN RECEPTIO
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| Cytoplasmic (Potential).
| Extracellular (Potential).
| Cytoplasmic (Potential).
| Cytoplasmic (Potential).
| Extracellular (Potential).
| Cytoplasmic (Potential).
| S-palmitoyl cysteine (Potential).
| S-palmitoyl cysteine (Potential).
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Matches
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wokin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Broak S.A., McZwan P.J., McKernan K.J., Malzek J.A., Gunaratne P.H.,
RA Hillon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha B.A., Mandan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Radiguez A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
And Forestion and initial analysis of more than 15,000 full-length human
361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLYYCIC 420
                                                                                                          RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC042416; AAH42416.1; -.
Neuropeptide; Receptor.
SEQUENCE 445 AA, 50726 MM; A2B0F3169DBA66BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                              421 HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                                                                                                                                                                                        HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
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Fri

430

300

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QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 190
                                                                                            251 GLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYSKKTACVLPAP 310
                                                  ERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK 370
                                                                                                                                                                             QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180
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                                                                                                              241 GLSNKENRLEENEMINLTLHPSRKIGPQVKLSGSHKWSYSFIKKHRRYSKKTACVLPAP
                                                                                                                                                                                                                        KRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL
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NA MEDIANCE FROW N.A.

SEQUENCE FROM N.A.

RA MEDIANE=21184976; PubMed=11287090;

RA MEDIANE=21184976; PubMed=11287090;

RT Cloning and characterization of the guinea pig neuropeptide Y

RT receptor YS.";

REMBL, AR362800.1;

RMBL, AR362800.1;

RMBL, AR36281; Cintegral to membrane; IEA.

RG, GO:0004983; F:neuropeptide Y receptor activity; IEA.

DR GO; CO:0004983; F:receptor activity; IEA.

DR GO; CO:0004887; F:receptor activity; IEA.

DR GO; CO:0004887; F:receptor activity; IEA.

DR GO; CO:0001884; F:rhodopsin-like receptor protein signalin. .;

DR GO; GO:0007186; P:C-Protein coupled receptor protein signalin.

DR InterPro; IPR000276; GPCR Rhodpsn.

DR InterPro; IPR000011; NPY_receptor.

DR InterPro; IPR000011; NPY_receptor.

DR InterPro; IPR000011; NPY_receptor.
                                   VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC
                                                                                                                                                                                                                                                                                                                                                                                               0925F1 PRELIMINARY; PRT; 446 AA.
0925F1;
0925F1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
NPY receptor 5.
Cavia porcellus (Guinea pig).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

94.0%; Score 2241; DB 2; Length 446;
Best Local Similarity 95.5%; Pred. No. 4.3e-141;
Matches 425; Conservative 10; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 AA; 50936 MW; 2C3984B0A90AA693 CRC64;
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PRINTS; PR00237; GPCRRHODPSN.
PRINTS; PR01016; NRPEPTIDEYSR.
PRNNTS; PR01012; NRPEPTIDEYR.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                           Receptor.
SEQUENCE
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REQUENCE FROM N.A.

REDINE=21184974; PubMed=11287088;

REDINES REDINES RECEPTOR OF RHESUS MONKEY NEUTOPEDIGE Y receptor

REDINES REDINES RECEPTOR RECEPTOR ACTIVITY; IEA.

REDINES REDINES RECEPTOR RECEPTOR ACTIVITY; IEA.

ROJ GO:0004983; F:neutopeptide signaling pathway; IEA.

ROJ GO:0007218; R:neutopeptide signaling RECEP-FI_2; I.

REMINTS; PRO1012; NRREPTIDEYR.

REMINTS; RRO1012; NRREPTIDEYR.

RW Neuropeptide; Receptor.

SEQUENCE 445 AA; SOBIZ MW; AEDACD2S9675BC93 CRC64;
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                            181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC
          VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC
                                                                        GLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYSKKTACVLPAP
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide Y receptor Y5.
Macaca mulata (Rhesus macaque).
Eukaryota; Metazoa; Croadata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
NCBI_TAXID=9544;
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Best Local Similarity 99.3%; Pred. No. 3.2e-146;
Matches 442; Conservative 2; Mismatches 1;
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Extracellular (Potential).
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      Cytoplasmic (Potential)
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Name=Npy5r; Synonyms=NPYR5;
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    TISSUE=Brain;
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121 QCVSVLVSTLILLISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180
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MEDLINE=99017319; Pubmed=9802393;
MEDLINE=99017319; Pubmed=9802393;
Borowsky B., Walker M.W., Bardd C.,
Vaysse P., Branchek T.A., Gerald C.,

"Molecular biology and pharmacology of multiple NPY Y5 receptor
species homologs";
T species homologs";
T species homologs ";
T species homologs activity seems to be associated with food intake. Could be involved in feeding disorders (By similarity).

-: SUBCELDULAR LOCATION: Integral membrane protein.

-: SUBCELDULAR LOCATION: receptors.

-: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

Highest to tachykinins receptors.
                                                                 VELQETFGSALLSSRYLCVESWFSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC
                                                                                                                             GLSNKENRLBENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAP
                                        VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQY1LPLVCLTVSHTSVCRSISC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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1 (Potential).
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15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5
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or send an email to license@isb-sib.ch)
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InterPro, IPR000276; GPCR Rhodpsn.
InterPro, IPR000393; NPY5_receptor.
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Canis familiaris (Dog).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                 Cytoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
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SCAC8D2FCF5D254A CRC64;
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3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential).
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                                                                                                            Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                          93.4%; Score 2227; DB 1;
94.8%; Pred. No. 3.7e-140;
ive 11; Mismatches 12;
                                                                                                                                                                                                                                                                        By similarity.
                                                                                                                                                                                (Potential)
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                      STRAINESPRAGUE-Dawley,

MEDLINE-96421636, pubMedes824284;

MEDLINE-96421636, pubMedes824284;

MEDLINE-96421636, pubMedes824284;

M. U. J. Bloomquist B.T., Confield L.J., Decarr L.B.,

H. U. J. Bloomquist B.T., Confield L.J., Decarr L.B.,

Rocaldowski, Y., Schaefer J., Velazquez N., McCaleb M.L.;

Rocaldowski, Y., Schaefer J., Velazquez N., McCaleb M.L.;

Tassociated with feeding behavior.";

J. Biol. Chem. 27126315-26319 (1996)

I. J. FORTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate of this receptor is mediated by G proteins that inhibit adenylate cyclass activity. Seems to be associated with food intake. Could be involved in feeding disorders.

C. I. SUBCELLULAR LOCATION: Integral membrane protein.

TISSUES PECIFICITY: Brain, hypothalamus.

C. I. MIRARIY: Belongs to family 1 of G-protein coupled receptors.

Highest to tachykinins receptors.
                Gerald C., Walker M.W., Criscione L., Gustafson E.L.,
Batzl-Hartmann C., Smith K.E., Vaysse P., Durkin M.M., Laz T.M.,
Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,
Taber R.I., Branchek T.A., Weinshank R.L.,
"A receptor subtype involved in neuropeptide-Y-induced food intake.";
Nature 382:168-171(1996).
                                                                                                                                                           Parker E.M., Babij C.K., Balasubramaniam A., Burrier R.E., Guzzi M., Parker E.M., Rukhopadhyay G., Rudinski M.S., Tao Z., Tice M., Xia L., Mullins D.E., Salisbury B.G.; analogues of the C-terminus of neuropeptide (122903) and other analogues of the C-terminus of neuropeptide Y are potent neuropeptide Y vare potent neuropeptide Y vare potent neuropeptide Y vareceptor agonists and neuropeptide Y vareceptor agonists.
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EMBL; U66274; AAC22845.1; --
EMBL; U66274; AAC22845.1; --
EMBL; U66274; AAC22845.1; --
EMBL; U66274; AAC22845.1; --
InterPro; IPR000236; UPV5_receptor.
InterPro; IPR00031; NPV_receptor.
InterPro; IPR0001; NPV_receptor.
InterPro; IPR000337; GPCRENDOPEN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
Phosphorylation; Transmembrane.
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[Voroplasmic (Potential).

[Voroplasmic (Potential).

Extracellular (Potential).

[Voroplasmic (Potential).

(Vroplasmic (Potential).

Extracellular (Potential).

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Extracellular (Potential)
7 (Potential).
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                                                                                                                                                    MEDLINE=98332165; PubMed=9669502;
   MEDLINE=96317589; PubMed=8700207;
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                                                                                                                                                                                                                                                         68 MGNLLILMAVMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKAMCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHSLVELGETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCR
                                                                                                                                                                                                                                                                                                                     MGNILLILMALMKKRNOKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDOWMFGKVMCHI
                                                                                                                                                                                                                                                                                                                                                                                                            MPFLQCVSVLVSTL1L1SIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV
                                                                                                                                                                                                                            QDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGF
                                                                                                                                                                                   Gaps
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STRAIN=129/Sv; TISSUE=Brain;
Chen H., Adams S., McWhinnie B., Bayne M., Gadski R., Zastawny R.;
Mouse neuropeptical Y Ys receptor characterized by repeat sequence
extracellular domain..;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99017379; PubMed=9802393;
MCDLINE=99017379; PubMed=9802393;
BOTOWSKY B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,
BOTOWSKY B., Branchek T.A., Gerald C.;
Vysse P., Branchek T.A., Gerald C.;
VMOlecular biology and pharmacology of multiple NPY YS receptor
  By similarity.
S-palmicoyl cysteine (Potential).
N-linked (GlcNAc. .) (Potential)
N-linked (GlcNAc. .) (Potential)
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                                                                                                                                       1; Length 456;
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070342; 035380; Q9JMK1;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor)
                                                                                                                                  87.4%; Score 2084.5; DB 1; Length
88.2%; Pred. No. 1.1e-130;
iive 22; Mismatches 30; Indels
                                                                                         MW; S157ABE341BA707E CRC64;
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                                                                                                                                  Query Match
Best Local Similarity 88.27
Matches 396; Conservative
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456 AA;
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAISS Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        REBL: ABBOIL346; BAA89531;

R MGD: MGI.108002; Nby5r.

R GO; GO:0016020; C:membrane; IDA.

GO; GO:0001602; F:pencreatic polypeptide receptor activity; IDA.

GO; GO:0001601; F:peptide YY receptor activity; IDA.

R InterPro; IPR00039; NPY5_receptor.

R InterPro; IPR00039; NPY5_receptor.

R PEAMYS; PR0001; Vtm.1; 1.

R PRINTS; PR0001; Vtm.1; 1.

R PROSITE; PS00237; GPRCRHODOPSN.

R PROSITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.

R G-protein coupled receptor: Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cycplasmic (Potential).

Cycplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Symilarity.

Cytoplasmic (Potential).

Noinked (GloNAc...) (Potential).

K -> Q (in Ref. 3).

W, B157F236EF2D4385 CRC64;
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Pred. No. 1.1e-129;
3; Mismatches 24;
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llarity 85.2%; Pre
Conservative 23;
                                                                                                                                                                                                                                                                                    EMBL; AF049329; AAC17839.1; -. EMBL; AF022948; AAB81829.1; -.
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length oDNAs.";
Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
STRARM-ESTBL/G7 IISSUE=Corpora quadrigemina;
MEDILINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Novmalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.",
LQYFLIGLYTFVSLLGFMGNLILIMAVMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTL
                                                           TSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFL
                                                                                       IATVWTLGFAICSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQ
                                                                                                                                                                 181 IATUWTLGFAICSPLPVFHSLVBLKETFGSALLSSKYLCVESWPSDSYRIAFTISLLLVO
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                                                                                                                                                                                                                      YILPLVCLTVSHTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSY
                                                                                                                                                                                                                                                                                                     SFIKKHRRRYSKKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEI
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Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
library, clone:B230213K17 product:NEUROPEPFIDE Y RECEPTOR TYPE 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
MEDIINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 NRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADLRALIHCLHM 465
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STRAIN=C57BL/6J; TISSUB=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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BAC32426;
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22; Gaps

Indels

49 9

----RNSDFPVWDDYKSSVDD

50 LQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTL 109

11 MDLELDEYYNKTLATENNTAAT-----

Similarity

Best Local S.W. Matches 397;

ò 엄 STANDARD;

NYSR

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Aizawa T., Harabizume W., A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hayashida K., Ishii Y., Itoh M., Kaqawa I., Kauda M., Kordo K., Konno H., Kondo M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nowaawa T., Mishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., A Saitoh H., Saitoh H., Sakazume N., Santo R., Saitoh H., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Asaski D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towa T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Sumitted (JUL-2001) to the EMBL/GenBank/DBBJ databases.

Meuropeptide: Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFIKKHRRRYSKKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEI 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOYFLIGLYTFVSILGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YILPLVCLTVSHTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                              SETRAINS—CSTRIVED; TISSUE=Corpora quadrigemina;
STRAINS—CSTRIVED; TISSUE=Corpora quadrigemina;
Shibata K. Itoh M. Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watahiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                       86.8%; Score 2070; DB 2; Length 466; 85.2%; Pred. No. 1.1e-129; ive 23; Mismatches 24; Indels 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRHFKLVYCI CHLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM
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                                                                                                                                                                                                                                                                                                                                                                                               52784 MW; B157F236EF2D4385 CRC64;
   Res. 10:1617-1630(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.2
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  466 AA;
                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide;
SEQUENCE 466
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). SEQUENCE PROM N.A.

STRAIN=LMD; TISSUE=Kidney;

ILO Y., Minezawa M.;

STRAIN=LMD; TISSUE=Kidney;

ILO Y., Minezawa M.;

ILO Y., Minezawa M.;

ILO Y., Minezawa M.;

STRAIN=LMD;

ILO Y., Minezawa M.;

ILO Y., Minezawa M.;

SUBMILLED GEORGE TO THE EMBL/Genbank/DDBJ databases.

ILO YOUNG (CCT-1998) to the EMBL/Genbank/DDBJ databases.

ILO YOUNG (CCT-1998) to the EMBL/Genbank/DDBJ databases.

ILO YOUNG TON: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate of cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).

ILO SIMILARITY: Belongs to family in G G-protein coupled receptors.

Highest to tachykinins receptors. Mraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P., Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P., Andersson L., Larhammar D., "Porcine NPY receptors NPYIR, NPY2R and NPY5R: cloning, mapping and Extracellular (Potential).

1 (Potential).

Cytoplasmic (Potential).

2 (Potential).

Extracellular (Potential).

3 (Potential).

Cytoplasmic (Potential).

4 (Potential).

5 (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

7 (Potential).

Cytoplasmic (Potential).

7 (Potential).

7 (Potential).

Nalinked (GlonAc...) (Potential).

Nalinked (GlonAc...) (Potential).

Nalinked (GlonAc...) (Potential).

Sysimilarity. Euteleostomi; Sus. Palmitate; S-palmitoyl cysteine (Potential). B7F616C2394C6CA0 CRC64; receptor) comparative analysis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases receptor). Name=NPYSR; Synonyms=NPYRS; Sus scrofa (Pig). Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 30-MAY-2000 (Rel. 39, Created) 30-WAY-2000 (Rel. 39, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Neuropeptide Y receptor type 5 (NPYS-R) (NPY-YS 50474 MW; 442 446 AA; 440 110 110 110 110 110 DOWAIN TRANSWEM DOMAIN TEANSWEM DOWAIN TRANSWEM TRANSWEM DOWAIN TRANSWEM DOMAIN TRANSMEM DOMAIN CARBOHYD LIPID SEQUENCE CARBOHYD

RESULT 9 NYSR_PIG

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70 57 130 116 190 176 250 236 310 296 369 356 429 416

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LILMALMKKRNOKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
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                                                                                                   11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
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                                                        Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vortebrata, Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
REQUENCE FROM N.A.
MEDLINE=98068842; PubMed=9407007;
Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of a novel neuropeptide Y receptor subtype in the zebrafish."; DNA Cell Biol. 16:1357-1363(1997).
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د
       Length 443;
                                                   Indels
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U-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Neuropeptide Y/peptide Y/ receptor Ya.
Name=npyrya; Synonyms=NPYRYA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ringvall M., Berglund M.M., Larhammar D., "Multiplicity of neuropeptide Y receptors: cloning
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Biochem. Biophys. Res. Commun. 241:749-755(1997).
     Score 1629.5; DB 2
Pred. No. 2.1e-100;
1; Mismatches 77;
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     68.3%; Scc
70.0%; Pre
tive 51;
                                                   310; Conservative
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01-AUG-1998 (TrEMBLrel.
                              Similarity
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SEQUENCE FROM N.A.
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Matches 31
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                     Gaps
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No. [1] SEQUENCE FROM N.A.

No. [2] Holmberg S.K.S., Mikko S., Boswell T., Zoorob R., Larhammar D.;

No. [2] Polarmacological characterization of cloned chicken neuropeptide Y receptors YI and YS.";

No. [2] Neurochem. 0.0-0(2003).

No. [3] ANG40844; AAR3556.1; -...

No. [4] GO: [6016021]; Cintegral ...

No. [6] GO: [6016021]; Cintegral ...

No. [7] GO: [6016021]; Fineuropeptide Y receptor activity; IEA.

No. [8] GO: [6001884]; Fineuropeptide Y receptor activity; IEA.

No. [6] GO: [6001884]; Fineuropeptide signaling pathway; IEA.

No. [7] GO: [7] No. [8] N
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0
  Length 446;
                                                   Indels
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PROSITE; PSSO425, G_PROTBIN_RECEP_F1_2; 1.
Neuropeptide; Receptor.
SEQUENCE 443 AA; 50044 MW; EFE9F1A391CC092E CRC64;
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Last annotation update)
  8; DB 1;
6.4e-127;
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                                                   34; Mismatches
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85.0%; Score 2028;
85.4%; Pred. No. 6.
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PRINTS, PR00237, GPCRRHODOPSN.
PRINTS, PR01016, NRPEPTIDEYSR.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
Neuropoptide Y receptor YS.
                         Best Local Similarity 85.4 Matches 380; Conservative
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ID Q8QFM2
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Salaneck E., Ardell D.H., Larson E.T., Larhammar D.; Three neuropeptide Y receptor genes in the spiny dogfish, Squalus acanthias, support en bloc duplications in early vertebrate evolution.";
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25-WAR-2004 (TrEMBirel, 27, Created)
25-WAR-2004 (TrEMBirel, 27, Last sequence update)
25-WAR-2004 (TrEMBirel, 27, Last annotation update)
NPY receptor YI (Fragment)
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                                                  Mol. Biol. Evol. 20:1271-1280(2003)
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                                                                                                                                                                                                                                                    23.4%; Score 558; DB 2; Length 377;
28.6%; Pred. No. 3.4e-29;
ative 68; Mismatches 136; Indels 106; Gaps
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Squalus acanthias (Spiny dogish).

Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Chondrichthyes;

Elasmobranchii, Squalea; Hypnosqualea; Squaliformes; Squaloidei;

Squalidae, Squalus.
                        42901 MW; _60E62AD9C7BFE5D0 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
     Brain Res. Mol. Brain Res. 70:242-252(1999).
EMBL; AF037400; AAC41276.1; -.
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SEQUENCE FROM N.A.
MEDLINE=22763539; PubMed=12777532;
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Best Local Similarity 28.6*
Matches 124; Conservative
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SEQUENCE 377 AA; 429
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52 GVSGNLLLITIIMKQXEMHNVTNILIVNLSVSDLLISVMCLPFTLVYTFMDHWIFGBAMC 111
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19 SERNFILD-NYDQCYSQTA-----------MIFTLALIYSAIIL
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22.1%; Score 527; DB 2; Length 348;
Best Local Similarity 25.7%; Pred. No. 3.6e-27;
Matches 115; Conservative 79; Mismatches 122; Indels 132; Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
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Squalus acanthias (Spiny dogfish).
Squalus acanthias (Spiny dogfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Squalidae, Squalus.
NCBI_TaxID=7797;
                                                                                 Squalus
                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Salameck E.W., Larson E.T., Ardell D.H., Larhammar D.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY177273; AAO62265.1;
EMBL; AY177272; AAO62265.1; JOINED.
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348 AA; 40738 MW; 817D35C53DAFD90F CRC64;
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Last annotation update)
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77 MKGRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVL 136
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MEDLINE-22763539; PubMed-12777532; Salaneck E., Ardell D.H., Larson E.T., Larhammar D.; "Three neuropeptide Y receptor genes in the spiny dogfish, sacanthias, support en bloc duplications in early vertebrate
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AAO62564;
25-MAR-2004 (TrEMBLrel. 27, Created)
25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
NPY receptor Y6.
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                                                                                                                       Mol. Biol. Evol. 20:1271-1280(2003)
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370 KKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCC 429
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26.4%; Pred. No. 7.8e-27;
tive 71; Mismatches 134; Indels 121; Gaps
Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NOBI_TaxID=7797;
                                                                                       SECURNCE FROM N.A.
MEDLINE=22763539; PubMed=12777532;
Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
araneck Neuropeptide Y Receptor Genes in the Spiny Dogfish, Squalus acanthias, Support en Bloc Duplications in Early Vertebrate
Evolution.";
Mol. Biol. Evol. 20:1271-1280(2003).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Salancek E.W., Larkammar D.; Salancek E.W., Larson E.T., Ardell D.H., Larkammar D.; Submitted (CGT-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY177271; AAO62564.1; -
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Best Local Similarity 26.49
Matches 117; Conservative
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SEQUENCE
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Search completed: October 21, 2004, 12:13:17 Job time : 193 secs

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(GGD2_6/ptodata1/iaa/5A_COMB.pep:*

(GGD2_6/ptodata71/iaa/5B_COMB.pep:*

(GGD2_6/ptodata71/iaa/6A_COMB.pep:*

(GGD2_6/ptodata71/iaa/BECOMB.pep:*

(GGD2_6/ptodata71/iaa/PCTUS_COMB.pep:*

(GGD2_6/ptodata71/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-200-673-64
US-09-194-895-4
US-09-194-895-4
US-09-147-907-4
PCT-US95-15646-4
US-08-630-1184A-6
US-09-003-1199-21
US-09-003-199-6
US-09-005-027-2
US-09-065-027-2
US-09-065-027-2
US-09-065-027-2
US-09-065-027-4
US-09-065-027-4
US-09-065-027-4
US-09-040-958-2
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-08-668-650B-2
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US-09-194-895-2
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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2385
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Match Length DB
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Perfect score:
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No.
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GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Garald, Christophe P.G.
APPLICANT: Malker, Mary
APPLICANT: Wainshank, Theresa
APPLICANT: Wainshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
TITLE OF INVENTION: DERROPEPTIDE Y/PEPTIDE YY RECEPTOR (YS) AND USES THERED;
MUNERS OF SEQUENCES:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CONTRESPONDENCE DUNHAM
STATE: New York
COUNTRY: United States of America
COUNTRY: United States of America
STATE: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDEY
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,025
                           PCT-US95-15646-2
US-08-630-118A-4
US-09-003-199-23
US-09-235-839-4
US-09-357-035-4
US-09-357-035-4
US-08-635-035-4
US-08-635-035-4
US-08-838-395-2
US-08-838-395-2
US-09-235-839-2
US-09-235-839-2
US-09-235-839-2
US-08-566-096A-6
US-08-566-096A-6
US-08-566-096A-6
US-08-566-096A-6
US-09-2447-907-6
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NAME: White, John P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-040
TELEFAX: (212) 391-0525
TELEX.X: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08349025 Patent No. 5602024
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APPLICANT: Gerald, Christophe P.G.
APPLICANT: Waker, Mary W.
APPLICANT: Water, Mary W.
APPLICANT: Water, Thereas
APPLICANT: Weinshank, Thereas
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: Methods of Modifying Feeding Behavior,
TITLE OF INVENTION: Compounds Useful In Such Methods, And DNA Encoding a
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                          KVMCHIMPPLOCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC
                                                                                                                              1 MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
                                                                                         Gaps
                                                                                         0
                                                     Length 455;
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                                                 100.0%; Score 2385; DB 2;
100.0%; Pred. No. 5.3e-180;
iive 0; Mismatches 0;
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CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: White Esq., John P.
REFISTRATION NUMBER: 26,678
REFERENCE/DOCKET NUMBER: 1795/46166C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orbania
SOFTWARE: Patenuia
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,650B
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08668650B
Patent No. 5989920
                                                                  al Similarity 100.
455; Conservative
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MEDIUM TYPE: Floppy
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Matches 455
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APPLICANT: Walker, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: METHODS OF MODIFYING PEEDING BEHAVIOR,
TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALA
TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (YS) AND USES THEREOF
                                                                                                                            180
                                                              61 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQMMFG 120
                                                                                                                                             CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 240
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                                                                                                                                                                                                                                                                                 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
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                                                                                                                       121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
PPELICATION NUMBER: US/08/566,096A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerald, Christophe P.G.
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US-08-566-096A-4
; Sequence 4, Application US/08566096A
; Patent No. 5968819
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TELEFAX: (212) 391-0525
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gerald
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APPLICANT: Weinshald, Christophe P.G.
APPLICANT: Weinshank, Richard L
APPLICANT: Weinshank, Richard L
APPLICANT: Weinshank, Theresa
APPLICANT: Wary M
APPLICANT: Branchek, Theresa
TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (YS)
FILE REFERENCE: 1795-4616-D-POTON JAMPABA
CURRENT APPLICANTON NUMBER: US/OS/194,895
CURRENT FILING DATE: 1990-09-27
PRIOR FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 24
SOSTWARE: Patentin Ver. 2.1
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                                                                                                                                                 1 MSFYSKODYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
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Best Local Similarity 100.0%; Pred. No. 5.3e-180;
Matches 455; Conservative 0; Mismatches 0;
                                             100.0%; Score 2385; DB 3;
100.0%; Pred. No. 5.3e-180;
ive 0; Mismatches 0;
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Patent No. 6531287
GENERAL INFORMATION:
                                                   Query Match
Best Local Similarity 100.
Matches 455; Conservative
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CRGANISM: Homo sapiens
US-09-194-895-4
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US-09-194-895-4
US-09-200-673-4
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APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Weinshank, Richard L.
APPLICANT: Walker, Mark Richard L.
APPLICANT: Walker, Mark Richard L.
APPLICANT: Walker, Mark W.
APPLICANT: Walker, Mark W.
APPLICANT: Walker, Mark W.
TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useft, TITLE OF INVENTION: ALYDICAL Neuropeptide Y/Peptide YY Receptor (YS)
TITLE OF INVENTION: ALYDICAL Neuropeptide Y/Peptide YY Receptor (YS)
TITLE OF INVENTION: ALYDICAL NEUROPER: US/09/200,673A
CURRENT FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-12-01
EARLIER FILING DATE: 1998-12-02
EARLIER FILING DATE: 1998-12-02
EARLIER FILING DATE: 1998-12-02
EARLIER FILING DATE: 1994-12-02
EARLIER FILING DATE: 1994-12-02
EARLIER FILING DATE: 1994-12-02
EARLIER FILING DATE: 1998-12-01
EARLIER FILING DATE: 1998-12-01
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EARLIER FILING DATE: 1998-12-02
EARLIER FILING DATE: 1998-12-02
EARLIER FILING DATE: 1998-12-01
EARLIER FILING DATE: 1998-12
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ilarity 100.0%; Pred. No. 5.3e-180;
Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPEAX: 212-39-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acids
                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-668-650B-4
                                                                                                                                                                                                                                                                                                            Similarity
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OY 181 CSPLPVPHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILELVCLTVS 240 181 CSPLPVPHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILELVCLTVS 240 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKGHRRRYS 300 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKGHRRRYS 300 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKGHRRYS 300 QY 301 KKTACVLPAPERPSQENHSRILPENFGSYRSQLSSSKFIPGVPTCFEIKPEENSDVHEL 360 DD 301 KKTACVLPAPERPSGENHSRILPENFGSYRSQLSSSKFIPGVPTCFEIKPEENSDVHEL 360 QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHIFHVYTDFNDNLISNRHFKLVYCIC 420 QY 421 HLLGWASCCLNPILYGFLNNGIKADLVSLIHCLHM 455 DD 421 HLLGWASCCLNPILYGFLNNGIKADLVSLIHCLHM 455 NBSSULT 7 US-09-447-907-4 ; Sequence 4, Application US/09447907 ; Patent No. 6645774	GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Gerald, Christophe P.G. APPLICANT: Walker, Mary W APPLICANT: Walker, Mary W APPLICANT: Branchek, Theresa ITLE OF INVENTION: And DNA Encoding A Hypothalamic Atypical Neuropeptide Y/Peptide Y FILE REFERENCE: 1795-46166CA CURRENT APPLICATION NUMBER: U590-411-23 PRIOR FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: 08/668,650 CURRENT FILING DATE: 1996-06-04 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin version 3:1 SEQ ID NO 4 LENGTH: 455 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: GORANISM: Artificial Sequence FEATURE: COTHER INFORMATION: Human Y5 CDNA clone	Query Match 100.0%; Score 2385; DB 4; Length 455; Best Local Similarity 100.0%; Pred. No. 5.3e-180; 0; Gaps 0; Matches 455; Conservative 0; Mismatches 0; 1ndels 0; Gaps 0; Qy I MSFVSKQDYMMDLELDEYYNKTLATENNYAATRNSDFPWHDDYKSSVDDLQYFLIGLYTF 60 1 Mismatches 0; 100.0%; Qy 61 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120 0 120 Qy 121 KVWCHIMPFLQCVSVLVSTLLISIAIVRYHMIKHPISNNLTANHGYPLIATVWTLGFAI 180 120 Qy 121 KVWCHIMPFLQCVSVLVSTLLISIAIVRYHMIKHPISNNLTANHGYPLIATVWTLGFAI 180 Qy 121 KVWCHIMPFLQCVSVLVSTLLISIAIVRYHMIKHPISNNLTANHGYPLIATVWTLGFAI 180 Qy 121 KVWCHIMPFLQCTSALLSSRYLCVESWPSDSYRIAFTISLLIQYILDFUCLIVS 240 Db 121 KVWCHIMPFLQCTSALLSSRYLCVESWPSDSYRIAFTISLLUQYILDFUCLIVS 240 Db 121 KVWCHIMPFLQCTSGALLSSRYLCVESWPSDSYRIAFTISLLUQYILDFUCLIVS 240 Db 241 HTSVCRSISCGLSKENRLEBENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300 Qy 241 HTSVCRSISCGLSKENRLEBNEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300 Qy 301 KKTACVLPAPERRSQENHSRILPENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300
DD 61 VSLIGFMGNLLILMALMKKRYQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120 QY 121 KVMCHIMPPLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180 121 KVMCHIMPPLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180 QY 181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 240 181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 240 QY 241 HTSVCRSISCGLSNKENRLEENEMINLTLAPSKKSGPQVKLSGSHKMSYSFIKKHRRRYS 300 QY 241 HTSVCRSISCGLSNKENRLEENEMINLTLAPSKKSGPQVKLSGSHKMSYSFIKKHRRRYS 300 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPERNSDVHEL 360 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPERNSDVHEL 360 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPERNSDVHEL 360 QY 421 HTGVMSCCLNPILVGFLNGIKADLVSLHCHM 455 DD 421 HLGMMSCCLNPILVGFLNNGIKADLVSLHCHM 455	SULT 6 Sequence 7, Application US/10013846 Sequence 7, Application US/10013846 Patent No. 6563367 APPLICANT: Bakthavatchalam, Rajagopal APPLICANT: Blum, Charles A APPLICANT: Brielmann, Harry L APPLICANT: Darrow, James W APPLICANT: De Lombært, Stephane APPLICANT: Tran, Jennifer APPLICANT: Tran, Jennifer APPLICANT: Tran, Jennifer APPLICANT: Tran, Sephane APPLICANT: Tran, Sephane APPLICANT: Tran, Sephane APPLICANT: Sheng, Xiaozhang APPLICANT: Sh	PRIOR FILING DATE: 2000-12-12 PRIOR PELICATION NUMBER: US 60/254,990 PRIOR FILING DATE: 2000-12-12 NUMBER OF SEC ID NOS: 17 SOFTWARE: PatentIn version 3.1 SEQ ID NO 7 TYPE: DRT ONEANISM: homosapiens US-10-013-846-7 OLENGTH: 455 TYPE: DRT US-10-013-846-7 OLENGTH: 455 MACCHES SIMILATICY 100.0%; SCORE 2285; DB 4; Length 455; Best Local Similatity 100.0%; Pred. No. 5.38-180; MACCHES 455; CONSELVATIVE 0, MISMARCHES 0; Indels 0, Gaps 0; MACCHES 455; CONSELVATIVE 0, MISMARCHES 0; Indels 0, Gaps 0; MASYSKODYNMDLELDEYYNKTLATENNYAATRNSDFPWDDYKSSVDDLOYFLIGLYTF 60 OV

m	CE	Qy 361 RVKRSVTRIKKRSRSVFYRLTILLILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420	QY 421 HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHW 455	RESULT 9 US-08-630-118A-6 ; Sequence 6, Application US/08630118A ; Patent No. 5519901	CENERAL INFORMATION: APPLICANT: Hu Ph.D., Yinghe APPLICANT: McCale Ph.D., Michael L.	T. Aime R. J.	; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid; TITLE OF INVENTION: Sequences	HUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff	STREET: 300 SOUTH WACKET DIIVE, 32110 FLOOL CITY: Chicago STATE: IL	COUNTRY: USA; ZIP: 60606	COMPUTER REAGALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	; OPERATING SYSTEM: PC-LOS/NS-LOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/630,118A FILING DATE: APTIL 8, 1996 GLASSIFICATION: 435	; ATTORNEY/AGENT INFORMATION: ; NAME: Greenfield Ph.D., Michael S. ; PRGISCHEATTON WINDER: 37.142	REFERENCE/DOCKET NUMBER: 96,149/WH 405; TELECOMMUNICATION INFORMATION: TELEPHONE: (312)715-1000	; TELEFAX: (312)715-1234 ; INFORMATION FOR SEQ ID NO: 6: ; SEQUENCE CHARACTERISTICS: . TENGTH: 445 amino acids	TYPE: amino acid	otein	Query Match 97.7%; Score 2330; DB 2; Length 445; Best Local Similarity 100.0%; Pred. No. 1.1e-175; Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFWGNL 70		Qy 131 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLFVFHSL 190
DD 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360	OY 361 RVKRSVTRIKKRSRSVFYRLTILIJVFAVSWMPLHLFHVYTDFNDNLISNRHFKLYVCIC 420 Db 361 RVKRSVTRIKKRSRSVFYRLTILIJVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420	Qy 421 HLLGMYSCCLNPILYGFLNNGIKADLVSLIHCLHM 455 Db 421 HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455	RESULT B PCT-US95-15646-4	; Sequence 4, Application PC/105915949 ; GENERAL INFORMATION: APPLICANT: Synaptic Pharmaceutical Corporation ; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS ; TITLE OF INVENTION: USBFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC ATYPIC ; TITLE OF INVENTION: VARBURDEN VES AND INSERT HERROF	TITLE OF INVENTION: Y/PEFILDE II RECEFICA (15) AND GES INDUCTOR (17) NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: COORET & Dunham LLP	STREET: 1185 Avenue of the Americas CITY: New York	COUNTRY: United States of America	865	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: PCT/US95/15646 ; FTLING DATE:	CLASSIFICATION: ATTORNATIONT INFORMATION: NAME: White. John P.	REGISTRATION NUMBER: 28,678 REFERENCE/COCKET NUMBER: 1795/46166-A-PCT	; TELEPHONE: (212) 278-0400 ; TELEPHONE: (212) 391-0525	; INPORMATION POR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: ; LENGTH: 456 amino acids	TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein	Query Match 100.0%; Score 2385; DB 5; Length 456; Best Local Similarity 100.0%; Pred. No. 5.4e-180;	Matches 455; Conservative 0; Mismatches 0; Indels 0; daps 1. Merocychovami el nevonvei amenumale PRINSPEDEMDIYKSSVDDLOYFLIGLYTE 60	.—Ēr	Qy 61 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSFFTLTSVLLDQMMFG 120	121		Qy 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRYS 300

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ADDRESSEE: Scher.
STREET: 2000 Gal.
CITY: Kenilworth
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                                                  VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC
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APPLICANT: Hu Ph.D., Yinghe
APPLICANT: How Ph.D., Michael L.
APPLICANT: Blooquist Ph.D., Brian T.
APPLICANT: Blooquist Ph.D., Jaime R.
APPLICANT: Plores-Riveros Ph.D., Jaime R.
APPLICANT: Plores-Riveros Ph.D., Jaime R.
APPLICANT: Neuropeptide Y Receptor and Nucleic Acid TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid TITLE OF INVENTION: Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.7%; Score 2330; DB 2; Length 445; 100.0%; Pred. No. 1.1e-175; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/838,399
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CLASSIFCATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION UNMBER: 37,147
REFERENCE, DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                NPILYGFLNNGIKADLVSLIHCLHM 455
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08838399
Patent No. 5965392
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 445; Conservative
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US-08-838-399-6
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1 MDLELDEYYNKTLATENNTAATRANSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60
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Patent No. 5985616
GENERAL INFORMATION:
PARKEY, Eric M
APPLICANT: Strader, Catherine D
APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY YS RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Schering-Plough Corporation
2000 Galloping Hill Road
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NAME: Thampoo., Immac J.
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CN07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)298-5061
TELEPAX: (908)298-5388
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MEDIUM TYPE: Diskette
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TELECOMMUNICATION INFORMATION:
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APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
TITLE OF INVENTION: Sequences
CORRESPONDENCE ADDRESS:
       Length 445;
                                          Indels
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COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive, 32nd Floor
         Score 2330; DB 2; I Pred. No. 1.1e-175;
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 97.7%; Score ... 100.0%; Pred. No. 1.10
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APPLICATION NUMBER: 08/630,118
FILING DATE: APPLISH 1996
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149-C
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Patent No. 6207799
GENERAL INFORMATION:
                                                445; Conservative
           Query Match
Best Local Similarity
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CITY: Chicago
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US-09-235-839-6
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Pred. No. 1.1e-175;
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ADDRESSEE: McDonnell Boehnen Hulbert
STREET: 300 South Wacker Drive
                                                                                                                                                                                               97.7%; Scor.
100.0%; Pred. No. ...
'-- 0; Mismatches
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; Sequence 6, Application US/09327035
; Patent No. 6368824
; GENERAL INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 445 amino acids TYPE: amino acid TOPOLOGY: linear
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 445; Conservative
                                                                                                                                         , MOLECULE TYPE: protein US-09-235-839-6
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STATE: IL
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Patentin Ver. 2.1
              ; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANTSM: Homo sapiens
US-09-065-027-2
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Best Local Simi
Matches 445;
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100.0%; Pred. No. 1.1e-175;
iive 0; Mismatches 0;
                                                                                                                       NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEPHONE: (312)715-1234
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09065027
Parent No. 652803
GENERAL INFORMATION:
APPLICANT: Herzog, H.
TITLE OF INVENTION: NEUROPEPTIDE Y-Y5 RECEPTOR
FILE REPERENCE: 273402001800
CURRENT APPLICATION NUMBER: US/09/065,027
CURRENT APPLICATION NUMBER: PCT AU96/00706
PRIOR APPLICATION UNMBER: PCT AU96/00706
PRIOR APPLICATION NUMBER: PCT AU96/00706
NUMBER OF SEQ ID NOS: 8
           APPLICATION NUMBER: US/09/327,035
FILING DATE: 07-Jun-1999
CLASSIFICATION: <UNKNOWN>
                                                           431 NPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                                                                                                                                                                                   LENGTH: 445 amino acids TYPE: amino acid
CURRENT APPLICATION DATA:
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Best Local Similarity 100.(
Matches 445; Conservative
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       Length 445;
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Similarity 100.0%; Pred. No. 1.1e-175;
45; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Maw, G
ITILE OF INVENTION: Pharmaceutical
FILE REFERENCE: PC1043AAM
CURRENT PEPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-01-07
PRIOR PILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-01-07
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PRIOR APPLICATION NUMBER: US 60/221,014
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/221,093
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Parentin Ver. 2.1
SEQ ID NO 13
LENGTH: 445
TYPE: PRI
CRGANISM: Homo sapiens
US-09-708-392-13
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Job time : 40 secs
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October 21, 2004, 12:07:45; Search time 129 Seconds (without alignments) 1141.939 Million cell updates/sec 2385 1 MSFYSKQDYNMDLELDEYYN.....GFLNNGIKADLVSLIHCLHM 455 1364641 segs, 323758627 residues OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-771-956-13 Perfect score: Scoring table: Searched: Sequence: Run on: Title:

1364641 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/PCT_REW_UBLPSPP:*
| cgn2_6/ptodata/1/pubpaa/PCT_REW_UBLPSPP:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 13, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 30, Appl	Sequence 7, Appli	Sequence 6, Appli	Sequence 205, App	Sequence 668, App	Sequence 14, Appl	Sequence 9, Appli	Sequence 533, App	Sequence 2, Appli	Sequence 4, Appli	
ID	US-09-771-956-13	US-09-962-646-4	US-10-013-846-7	US-10-410-648-7	US+09-771-956-30	US-10-274-851-7	US-10-027-049-6	US-10-225-567A-205	US-10-295-027-668	US-10-181-906-14	US-09-771-956-9	US-09-826-509-533	US-09-962-646-2	US-10-027-049-4	
DB	σ	σ	14	15	σ	14	14	14	14	15	σ	10	σ	14	
Query Match Length DB ID	455	455	455	455	455	455	445	445	445	445	499	445	456	445	
Query	100.0	100.0	100.0	100.0	99.5	99.3	7.76	7.76	97.7	7.76	97.5	97.3	87.4	87.0	
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14 US-10-027-049-2	US-09-771-95	09-771-95	US-09-962-64	US-09-771-956-	9 US-09-771-956-10	4 US-10-013-846	0-410-64	4 US-10-274-	US-09-771-956-2	US-09-771-9	-771-956-2	US-09-771-956-	US-09-771-956-2	US-09-771-95	4 US-10-081-810	US-09-771-95	9-393-69	4 US-10-013-84	10-176-8	4 US-10-225-567A-	US-10-309-51	US-10-177-	US-10-060-369-1	US-10-291-990-	US-10-126-764-1	-10-295-027-64	US-10-295-027-7	US-10-410-648-	-10-181-9	US-10-081-810
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ALIGNMENTS

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61 VSLIGFMGNILILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120
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                                                                                                                          APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
FILE REFERENCE: N2000.001
CURRENT PILING DATE: 2001-01-29
NUMBER OF SOG ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.13
LENGTH: 455
TYPE: PRT
                                                Sequence 13, Application US/09771956; Patent No. US20010031474A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
RESULT 1
US-09-771-956-13
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Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL 360 Qy 361 RVKRSVTBIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420	APPLICANT: Bakthavatchalam, Rajagopal APPLICANT: Blum, Charles A APPLICANT: Blum, Charles A APPLICANT: Blum, Charles A APPLICANT: Blum, Charles APPLICANT: Brielman, Harry L APPLICANT: Darrow, James W APPLICANT: Tran, Jennifer APPLICANT: Tran, Jennifer APPLICANT: Tran, Jennifer APPLICANT: Elliott, Richard L APPLICANT: Bliott, Richard L APPLICANT: Solor 2001 CURRENT APPLICATION NUMBER: US/10/013,846 CURRENT FILING DATE: 2000-12-12 CURRENT APPLICATION NUMBER: US 60/254,990 PRIOR FILING DATE: 2000-12-12 PRIOR FILING DATE: 2000-12-12 SOFTWARE: PatentIn version 3.1 SEQ ID NO 7 LENGTH: 455 TYPE: PRT CREANISM: homosapiens US-10-013-846-7	Query Match 100.0%; Score 2385; DB 14; Length 455; Best Local Similarity 100.0%; Pred. No. 1e-191; Andels 0; Gaps 0; Matches 455; Conservative 0; Mismatches 0; Gaps 0; Qy 1 MSFYSKODYMMDLELDEYNKTLATENNADEPPWADDYKSSVDDLQYFLIGLYTF 60 60 GI VSLLGFMGNLLILMALWKKRNOKTTVNFLICNLAFSDILVVLFCSPFTLTSVLLDQWFG 120 Qy 61 VSLLGFMGNLLILMALWKKRNOKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWFG 120 GI VSLLGFMGNLLILMALWKKRNOKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWFG 120 Qy 121 KVMCHIMPPLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180 Qy 121 KVMCHIMPPLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180 Qy 181 CSPLPVFHSLVELGETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILEPLVCTTVS 240 Qy 241 HTSVCRSISCGLSNKENRLEENBEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKGHRRYS 300 Qy 301 KKTACVLPAPERPSQENHSRILDENFGSVRSQLSSSKFIPGVPTCFEIKPEENSDVHEL 360 Qy 361 RVKRSVTRIKKRSRSRSVPYRLTILILVVPAVSWMPLHFHVVTDFNDNLISNRHFKLVYCIC 420
Db 181 CSPLPVFHSLVELGETFGSALLSSRYLCVESMPSDSYRIAFTISLLLVQYILPLVCLTVS 240 Qy 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKMSYSFIKKHRRRYS 300 241 HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKMSYSFIKKHRRRYS 300 Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDYHEL 360 Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDYHEL 360 Qy 361 RVKRSVTRIKKRSRSVFYRLTILILVPAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420 Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420 QY 421 HLGMMSCCLNPILYGFLANGIKADLCHHM 455	PDb 421 HLLGWMSCCLNPILYGFLNNGIKÄDLVSLÄHÖLÄM 455 RESULT 2 US-09-962-646-4 i Sequence 4, Application US/09962646 i Sequence 4, Application US/09962646 i Patent No. US20020103123A1 i GENERAL INFORMATION: APPLICANT: WEINSTAUN, RICHARD L. APPLICANT: WEINSTAUN, ROUPTING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE YY RECEFFILE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE YY RECEFFILE REFERENCE: 1795/461662A CURRENT APPLICATION NUMBER: US/09/962,646 CURRENT APPLICATION NUMBER: 08/566,096 PRIOR APPLICATION NUMBER: 08/566,096 PRIOR APPLICATION NUMBER: 08/566,096 PRIOR PILING DATE: 1999-12-01 PRIOR PILING DATE: 1994-12-01 NUMBER OF SEQ ID NOS: 17 AOFTWARP: Datenty vareion 11 AOFTWARP: Datenty vareion 11 AOFTWARP: Datenty vareion 11	SEQID NO 4 Incomparison of the Comparison of th

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APPLICANT: Blum, Charles A.
APPLICANT: Blum, Charles A.
APPLICANT: Blum, Charles A.
APPLICANT: Blum, Charles A.
APPLICANT: Darrow, James W.
APPLICANT: De Lombaert, Stephane W.
APPLICANT: Tram, Jennifer W.
APPLICANT: Tram, Jennifer W.
APPLICANT: Tram, Jennifer W.
APPLICANT: Tram, Jennifer W.
APPLICANT: Alliot, Richard L.
APPLICANT: APPLICANT: Bliott, Richard L.
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APPLICANT: APPLICANT: Bliott, Bliott
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421 HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455 | HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455 | 421 HILGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM 455
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                                                                                                                                                                                                                                                  Sequence 7, Application US/10410648
, Publication No. US20040072847A1
, GENERAL INFORMATION:
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ORGANISM: homo sapiens
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APPLICANT: Brielmann, Harry
APPLICANT: Brielmann, Harry
APPLICANT: De Loombeart, Stephane
APPLICANT: De Loombeart, Stephane
APPLICANT: The OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE
TITLE OF INVENTION: DERIVATIVES
FILE REFERENCE: U 014209-8
CURRENT APPLICATION NUMBER: US/10/274,851
CURRENT FILING DATE: 2002-10-21
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99.5%; Score 2373; DB 9; Length 455;
Best Local Similarity 99.3%; Pred. No. 1e-190;
Matches 452; Conservative 2; Mismatches 1; Indels
RESULT 5
US-09-771-956-30

Sequence 30, Application US/09771956

Patent No. US20010031474A1

GENERAL INFORMATION:
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
FILE REFERENCE: N2000.001

CURRENT FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 31

SECTIMARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 455
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ATTORNEY/AGENT
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                                                                                                                                                            Gaps
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McCaleb Ph.D., Michael L.
Bloomquist Ph.D., Brian T.
Flores-Riveros Ph.D., Jaime R.
Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuroperide Y Receptor and Nucleic Acid
                                                                                                                                                            0;
                                                                                                                             Length 455;
                                                                                                                                                            Indels
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CORRESPONDENCE ADDRESSE:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: 1L
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDMER: US/10/027,049
FILING DATE: 08-Apr-1996
                                                                                                                           Score 2368; DB 14;
Pred. No. 2.7e-190;
0; Mismatches 2;
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                                                                                                                           99.3%;
               SOFTWARE: Patentin Ver. 2.0
                                                                                                                      Query Match
Best Local Similarity 99.6
Matches 453; Conservative
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NUMBER OF SEQ ID NOS: 17
                                                                           ; ORGANISM: Homo sapiens
US-10-274-851-7
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                            SEQ ID NO 7
                                                             TYPE: PRT
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US-10-225-567A-205

Sequence 205, Application US/10225567A

Sequence 205, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: B
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                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 96,149/WH
TELECOMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                         NAME: Greenfield Ph.D., Michael
REGISTRATION NUMBER: 37,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-027-049-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 NPILYGFLNNGIKADLVSLIHCLHM 445
CLASSIFICATION: <Unknown>
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                             11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
                                                                                                           Gaps
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0
                                                                Length 445;
                                                                                                      0; Indels
                                                            97.7%; Score 2330; DB 14;
100.0%; Pred. No. 4.1e-187;
tive 0; Mismatches 0;
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Matches 445; Conservative
, ORGANISM: Homo sapiens
US-10-225-567A-205
                                                                Query Match
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RESULT 9
US-10-295-027-668
US-10-295-027-668
Sequence 668, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Aziz, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Matson, Susan R.
APPLICANT: Bos Blotechnology, Inc.
ITTLE OF INVENTION: Methods of Ecreening for Modulators of Cancer
ITTLE OF INVENTION: Methods of Soft Diagnosis of Cancer
ITTLE OF INVENTION: WHORER: US 10/10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PAPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-13
PRIOR PAPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-12
PRIOR PLING DATE: 2001-11-29
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US-10-181-906-14
; Sequence 14, Application US/10181906
; Publication No. US20040D53864A1
; GENERAL INFORMATION:

APPLICANT: Karsenty, Gerard
APPLICANT: Karsenty, Gerard
APPLICANT: Amling, Michael
APPLICANT: Amling, Michael
APPLICANT: Amling, Michael
APPLICANT: Description
TITLE OF INVENTION: MCDULATION OF NEUROPEPTIDE Y ACTIVITY
TITLE OF INVENTION: MCDULATION OF NEUROPEPTIDE Y ACTIVITY
FILE REFERENCE: 9142-020-999
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US/10/181,906
PRIOR PELING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NO 14
LENGTH: 445

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PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-00
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR PLING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 97.7%; Score 2330; DB 14; Length 445; al Similarity 100.0%; Pred. No. 4.1e-187; 445; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                   t TYPE: PRT
CORGANISM: Homo sapiens
US-10-295-027-668
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   SEQ ID NO 668
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Sequence 533, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lihaw, Chen W.
TITLE OF INVENTION:
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF EG ID NOS: 589
                                                             KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180
                                                                                                                                    CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 240
61 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120
                                                                                                                                                                                     HISVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYS 300
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                                                                                                                                                                                                                                                              KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL
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Pred, No. 2.3e-186;
0; Mismatches 1;
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Best Local Similarity
Matches 444; Conserv
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                                                                                                                                           11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
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0
                                                                      Length 445;
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99.6%; Pred. No. 1e-186;
tive 1; Mismatches 1; Indels
                                                                                                          0; Indels
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Patent No. US20010031474A1
GENERAL INFORMATION:
APPLICANT: Bennett, Michele
APPLICANT: Reause, James
TILE OF INVENTION: Chimeric Neuropeptide Y Receptors
TILE OF INVENTION: Chimeric Neuropeptide Y Receptors
TILE REFERENCE: N2000.001
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                 97.7%; Score 2330; DB 15;
100.0%; Pred. No. 4.1e-187;
ive 0; Mismatches 0;
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                                                                                    Best Local Similarity 100.
Matches 445; Conservative
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         ORGANISM: Homo sapiens
US-10-181-906-14
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US-09-771-956-9
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                                                                     Query Match
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367 TRIKKRSRSVFYRLTILILVFAVSWMPLHVFHVVTDFNDNLISNRHFKLVYCICHLLGMM 426
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                                                                                                                                                                                                                                                                    Sequence 4, Application US/10027049
Publication No. US2003002283A1
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
McCaleb Ph.D., Michael L.
Bloomquist Ph.D., Brian T.
Flores-Riveros Ph.D., Jaime R.
Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 2074.5; DB 14; Length 445; 88.5%; Pred. No. 1.2e-165; tive 21; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

PAPLICATION NUMBER: US/10/027,049
FILING DATE: 08-Apr.-1996
CLASSIFICATION: «Unknown»
ATTOREY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REGISTRATION NUMBER: 96,149/WH 405
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                      427 SCCLNPILYGFLNNGIKADLRALIHCLHM 455
                                                                                         427 SCCLNPILYGFLNNGIKADLVSLIHCLHM 455
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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US-10-027-049-4
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Patent No. US20020103123A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT GERLD, CHRISTOPHE P.G.
APPLICANT WALKER, MARY W
APPLICANT BRANCHEK, THEREA
TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATVPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEF
FILE REFERENCE: 1795/46166EZA
CURRENT APPLICATION NUMBER: US/09/962,646
CURRENT FILING DATE: 2001-09-24
PRIOR PRILOR APPLICATION NUMBER: 08/566,096
PRIOR APPLICATION NUMBER: 08/566,096
PRIOR PELING DATE: 1998-11-25
PRIOR PELING DATE: 1998-11-25
PRIOR PELING DATE: 1998-12-01
PRIOR FILING DATE: 1998-12-01
NUMBER: 08/549,025
PRIOR FILING DATE: 1994-12-01
NUMBER: 08/49,025
NUMBER: 08/49-10-01
NUMBER: 08/49-10-01
NUMBER: 08/49-10-01
                                                                                                                                                                                      371 KRSRSVFYRLTILILVPAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 430 [][][][][][][][][][][][][][][][][][]]]361 KRSRSVKYRLTILILVFAVSWMPLHLFHVYTDFNDNLISNRHFKLVYCICHLLGMMSCCL 420
311 ERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK 370
                                                                                                                                    301 ERPSÓENHSRILDENFGSVRSÓLSSSSKFIPGVPTCFFIKPEENSDVHELRVKRSVTRIK 360
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87.4%; Score 2084.5; DB 9; Length
Best Local Similarity 88.2%; Pred. No. 1.8e-166;
Matches 396; Conservative 22; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                Sequence 2, Application US/10027049
Publication No. US20030022283A1
GENERAL INFORMATION:
APPLICANT: HU Ph.D., Yinghe
MCCaleb Ph.D., Michael L.
Flores-Riveros Ph.D., Daime R.
Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.7%; Score 2067.5; DB 14; Length 445; ilarity 88.3%; Pred. No. 4.6e-165; Conservative 21; Mismatches 30; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,049
FILING DATE: 08-Apr-1996
CLASSIFCATION: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REFERENTON NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: iL
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**MOLECTIA TYPE: protein

**SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-027-049-2
                                                                                                                                                                             NPILYGFLNNGIKADLVSLIHCLHM 455
                                                                                                                                                                                              Floppy disk
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 393; Conserv
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US-10-027-049-2
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YS receptor; atypical neuropeptide Yl receptor; feeding behavior; G protein-coupled receptor; agonist; antagonist; obesity; bulimia; anorexia; transgenic animal.
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88. .110
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126. .147
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AAY52578

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AAF25577

AAW29412

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    Aav25939 Human Y5
Aaw29447 Human hip
Aaw37093 Human hip
Aay37093 Homo sapi
Aay57461 Human hip
Aae08002 Human neu
Abb64497 Human neu
Abo53266 Human neu
Aac23266 Human neu
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                 protein search, using frame_plus_n2p model
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Fgapop 6.0, Fgapext (
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                                                                 ATTITAATATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT
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                                                                                                                                                                                                                                                                                                                Modifying feeding behaviour using Y5 receptor (ant)agonists - increases or decreases food consumption, for treatment of e.g. obesity or bulimia
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                                                 AsnGlnLysThrThrValAsnPheLeulleGlyAsnLeuAlaPheSerAsplleLeuVal
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                                                                                                                                                                                                                                                                                                                                           Use of new and known quinazolin-2,4-diazirine compounds as NPY Y5 receptor antagonists - for treating and preventing eating disorders, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGACACTIGCCACAGAGAATAATACTGCCACTCGGAATTCTGATTTCCCAGTCTGG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                         Human hippocampal neuropeptide Y Y5 receptor
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421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProlleLeuTyrGlyPheLeuAsnAsn 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of new and known hetero:aryl compounds as NPY Y5-receptor antagonists - for treating and preventing eating disorders, diabetes, dyslipidaemia, hypertension, memory loss, epilepsy, migraine, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents human hippocampal neuropeptide (NP) Y receptor subtype Y5, with a pharmacological function associated with for example, obessity and eating disorders. The specification relates to a method of treatment and prophylaxis of disorders and diseases associated with with NPY receptor subtype Y5 comprising administering to a warm-blooded animal, including man, in need of such treatment a therapeutically effective amount of a new heteroaryl compound. These disorders and diseases include e.g. eating disorders, obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, pain, sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage, shock, congestive heart failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                     Human hippocampal neuropeptide Y Y5 receptor, NPY Y5, prophylaxis, bulimia nervosa; diabbetes; dyslipidaemia; hypertension; memory loss; epileptic siezure; migraine; sleep disturbance; pain; depression; sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea; congestive heart failure; eating disorder; obesity.
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Tintelnotblomley M, Schilling W, Criscione L;
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                                                                    AAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCCAGTCTGG
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                                                                     ACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGATTTGCATTTGT 1276
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                                                                                                              CATITICITICGCCATGATGTCCTGTTGTCTTAATCCAATTCTATATGGGTTTCTTAATAAT
                                          ThrileLeuileLeuvalPheAlaValSerTrpWetProLeuHisLeuPheHisValVal
                                                                                  Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity; feeding behaviour; modification; atypical neuropeptide.
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                                                                                                                                                                GlylleLysAlaAspLeuValSerLeulleHisCysLeuHisMet 455
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N-PSDB; AAV00622.
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                                                           AGAGTAAAAACGTTCTGTTACAAGAATAAAAAAAAAGAGATCTCGAAGTGTTTTCTACAGACTG
                                                                                                ThrileLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal
                                                                                                                     ACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCATTTGT
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The present sequence represents the human hippocampal Y5 receptor. The Y5 receptor is a G-protein coupled neuropedide Y receptor found throughout the mammalian nervous system and is a powerful stimulant of feeding behaviour. Cells expressing DNA encoding the Y5 receptor can be used to determine whether a ligand specifically binds to a Y5 receptor. These cells or a cell extract, is exposed to the ligand and then any binding between the ligand and the receptor can be detected. The cells can also be used to determine whether a ligand is a Y5 receptor can also agonist. The binding of chemical compounds to a Y5 receptor can also determined and whether they activate or inhibit the activation of the Y5

Disclosure; Fig 6; 87pp; English.

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receptor can also be determined using cells expressing the receptor. The effect of drugs on the Y5 receptor and whether they act as agonists or antagonists can also be detected with these cells
                                                                                                                                                                                                                                                                                          1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn
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281 LeuSerGlySerHisLysTrpSerTyrSerPhelleLysLysHisArgArgArgArgTyrSer 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein, transmembrane; TM domain, therapy, obesity; blood pressure; eiplepsy; Huntington's disorder; Parkinson's disorder; sating disorder; selzure; locomotor; anxiety disorder; limbic seizure; tranquilliser; human
                                                                 917 AAGAAGACAGCATGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA
                                                                                                    ATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTCATA
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221. .241
/note= "Fifth TM domain"
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/note= "Second intracellular loop domain'

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    /note= "N-terminal extracellular domain"

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/note= "Second TM domain"
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/note= "Fourth TM domain"
189. .220
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/note= "First TM domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neuropeptide Y5 (NPY5) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPYS receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is human NPYS receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 AAGACACTIGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCAGTCTGG 136
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                                                                                                                                                                                                                                                                                                                                                                                                       New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development.
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             "Third intracellular loop domain"
                                                                                                                                        "C-terminal intracellular domain"
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Matches:
Conservative:
Mismatches:
Indels:
                                                          402. .414
/note= "Third extracellular
                                                                                                   /note= "Seventh TM domain"
439. .455
                                             "Sixth TM domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 55-56; 72pp; English
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Best Local Similarity:
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257 AATCAGAAGACTACGGTAAACTTCCTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTT 316

61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg

197 GIAAGICTICTIGGCTITATGGGGAATCTACTTATTAATGGCTCTCATGAAAAGCGT

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196

41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeulleGlyLeuTyrThrPhe 60

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AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
                                                                                                                                                                                                                                    LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
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                                                CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla
                              GTGCTGTTTTGCTCACCTTTCACACTGACGTCTGTCTTGCTGGATCAGTGGATGTTTGGC
                                                                                         ATTITAATATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT
                                                                                                                                                                                                               TTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTCTGGACACTAGGTTTTGCCATC
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This invention describes a novel method of modifying feeding behaviour of a subject which is a Y seceptor agonist or antagonist effective to compound which is a Y seceptor agonist or antagonist effective to increase or decrease, respectively, the consumption of food by the subject so as to modify feeding behaviour of the subject. The product of the invention has metabolic, anotectic, antidepressant, tranquiliser, antidiarabeic and heemostatic activity and can be used in a vaccine. Ys receptor agonist or antagonist compounds are useful for treating a nathormality alleviated by the inhibition or activation of Ys reacting an abnormality alleviated by the inhibition or activation of Ys receptor, in a subject. Antibodies raised against the receptor are useful for treating an abnormality alleviated by the inhibition or activation of Ys receptor, in a subject. Antibodies raised against the receptor are useful for detecting the presence of the receptor on the surface of a call. The agonist of X receptor is useful for treating an abnormality in a subject, where the abnormality includes anoreal productive disorder, depression, anxiety, memory loss, migraine, pain, epileptic seizure, hypertension, cerebral haemorrhage, shock, congestive heart failure, bleeve disturbance, nasal congestion, and diarrhoea. This sequence represents the human hippocamus YS receptor described in the
                                                                                                                                                                              Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor; food consumption; metabolic, anorectic; antidepressant; tranquiliser; antimigratine; analgesic; hypotensive; cerebroprotective; cardiant; antidiarrhoeic; haemostatic; vaccine; anorexia; obesity; bulimia; sexual disorder; reproductive disorder; depression; anxiety; memory loss; migranne; pain; epileptic seizure; hypertension; cerebral haemorrhage; shock; congestive heart failure; sleeve disturbance; nasal congestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying feeding behavior of subject, useful in treating feeding disorders, involves administering to subject Y5 receptor agonist or antagonist, to increase or decrease consumption of food by subject.
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Matches:
Conservative:
                                                                                                                                                       Human hippocampus Y5 receptor protein.
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                                     ABB84497 standard; protein; 455
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95US-00566096.
98US-00200673.
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Percent Similarity:
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01-DEC-1995;
25-NOV-1998;
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                                                                                                                  20-DEC-2002
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                                                                            ABB84497;
RESULT 7
ABB84497
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	s41 FrociyvalFrointCysFneGi	Qy 1097 AcaGIAAAACGITCIGITACAAGAAIAAAAAGAAATCIG 	Oy 1157 ACCATACTGATATTAGTATTTGCTGTTAGTTTGGATGCCAC	Qy 1217 ACTGATTTTAATGACAATCTTATTTCAAATAGGGATTTC	401	Qy 1277 CATTIGITGGGCATGATGTCCTGTTGTCTTAATCCAATTC	Qy 1337 GGGATTAAAGCTGATTTAGTGTCCCTTATACACTGTCTTC		RESULT 8 ABB79510 ID ABB79510 standard; protein; 455 AA. XX	AC ABB79510; XX TY 23.cmp_2002 (fixet entwy)	23-25F-2002 (LIESU Human Deutropeptide Y		KW hypotensive; antidiabetic; psychiatric; anticonving cerebroprotective; antidepressant; haemostatic; KW neuroleptic; antidanginal; nephrotropic KW gastrointestinal; antiasthmatic.		PN WO200248152-A2. XX	PD 20-JUN-2002. XX PP 11-PEC-2001. 2001WO-HS047863.	12-DEC-2000; 2000US-0254990	XX PA (NEUR-) NEUROGEN CORP.	AA PI Bakthavatchalam R, Blum CA, Brielmann HL, Darr PI De Lombaert S, Hutchison A, Tran J, Zheng X, XX	DR WPI; 2002-547845/58. DR N-PSDB; ABN84252.	XX PT New substituted spiro(isobenzofuran-1,4'-piperidi PT spiroisobenzofuran-1,4'-piperidine, useful for tx			the present sequence is the procein sequence for CC Y5 (MPY5) receptor. In an example from the invention including human NPY5 receptor sequences were cons		
Similarity: 100.00% Mismatches: 0 1: Indels: 0 5 Gaps: 0	956-4 (1-1406) x ABB84497 (1-455)	17 AIGTCTTTTATTCCAAGCAGCAGCATATAATATGGATTTAGAGCTCGAGGATATTATAAC 76	AAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCAGTCTGG	LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp	onto the control of the control	GTAAGTCTTCTTGGCTTTATGGGGAATCTACTTATTTTAATGGCTCTCATGAAAAGCGT	1 ValSerLeubeuGiyPheMerGiyAsnLeubeulleLwetAlaLeuMetLysbysArg	STATE STAT	317 GTGCTGTTTTGCTCACCTTTCACACTGACGTCTTGCTGGATCAGTGGATGTTTGGC 376	AAAGICANGIGCCATATTATTGCCTTTTTCTAATGTGTGAGTTTTGGTTTTAACTTTA 4	17- 17- 17-	437 ATTTPATATCAATTGCCATTGTCAGGATCATATGATAAAACATCCCATATCTAATAAT 496 	497 TTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTCTGGACACTAGGTTTTGCCATC 556	57 IGTTCTCCCCTTCCAGIGTTTCACAGICTIGIGAAACTTCAAGAAACAITTIGGTTCAGCA	CysserProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla	617 TIGCTGAGCAGCATATTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCC 676 [TTACTACTACTTATTGCTAGTATATTGCCGTTAGTTAGTT		737 CATACAAGTGTCTGCAGAAGTATAAGCTGTGGATTGTCCAACAAGAAAAGAGACTTGAA 796 	GAAAATGAGATCAACTCTAACTCTTCATCAAAAAGAGTGGGCTCAGGAAA	261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysLysSerGlyProGlnValLys 280	857 CTCTCTGGCAGCCATAAATGGAGTTATTCATTCATCAAAAAACACAGAAGATATAGC 916	I DEGOGLETYOOTUIDEDARIIDAGETIATOOTUIDAGETETTETTETTETTATAATOOTUIDIATOOTU	301 LystysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAshHisSerArg 320	77 ATACTICCAGAAAACTITGGCTCTGTAAGAAGTCAGCTCTTTCATCCAGTAAGTTCATA	alArgSerGinLeuSerSerserLysPh
Best Local S Query Match: DB:	US-09-771	\(\delta \)	ì ò	a 8	S 8	ð í	g à	g g	λς qα	, VQ	qq	Qy QD	\chi_{\delta}	ζ	원	λό qa	ζō	qa	Oy Db	٨٥	Dþ	δ _γ	2 6	e do	Qy	QQ

TTCGAAGTGTTTTCTACAGACTG 1156 ACTACACCTTTTCCATGTGGTA 1216 CCAAGTIGGIGIATIGCAITIGI 1276 TTCTATATGGGTTTCTTAATAAT 1336 for the human neuropeptide vention, chinaric receptors constructed, and used to e invention. Substituted d 3H-spivoisobenzofuran-1,4' tora activity are provided. binding to NPYS receptors Irrow JW; Elliott RL, Hammond M; antagonist, anorectic; cardiovascular; onvulsant, cardiant, c; tranquillizer; opic; uropathic; din)-3-one or 3H-treating, e.g. eating or diabetes. TTCATATG 1381 ||||||||| euHisMet 455

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Neuropeptide Y5; receptor; NPY5; 2-cyclohexyl-4-phenyl-1H-imidazole; NPY; appetite regulation; feeding disorder; obesity; bulimia; diabetes; psychiatric; cardiovascular; hypertension; cerebral infarction; epilepsy; schlzophrenia; depression; angina; sudden cardiac death; vasospasm; arrhythmia; utinary incontinene; Crohn's disease; asthma; neuroleptic; antiinflammatory; nootropic; vasotropic; anticonvulsant; uropathic;
                              LeuSerGlySerHisLysTrpSerTyrSerPhelleLysLysHisArgArgArgTyrSer
                                                                                                                                                         ATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTTCATCCAGTAAGTTCATA
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in vivo or in vitro, and are particularly useful in the treatment of a variety of disorders, e.g. eating disorders such as obesity or bulimia, psychiatric disorders, diabetes and cardiovascular disorders such as hypertension, in humans and animals
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This invention relates to novel ligands (derivatives of 2-cyclohexyl-4-phenyl-1H-inidazole) for the neuropeptide Y5 (NPY5) receptor. The NPY5 receptor mediates a variety of physiological effects and is involved in appetite regulation, hormone release and blood pressure. Ligands that modulate the NPY5 receptor inhibit or enhance NPY binding such that they can be used to treat a variety of conditions including feeding disorders (obesity and bulinia), psychiatric disorders, diabetes and cardiovascular diseases such as hypertension. Further uses relate to to the treatment of cerebral infarction, epilepsy, schizophramia, despession, angina, sudden cardiac death, vasospasm, arrhythmia, urinary incontinence, Crohn's neuroleptic, antilniflammatory, nootropic, vasotropic, anticonvulsant and uropathic. This polypeptide sequence is the human neuropeptide Y5 (NPY5) receptor protien of the invention
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Matches:
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Mismatches:
Indels:
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                                     Example 10; Page 39-41; 63pp; English.
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TIGCTGAGCAGCAGGTATITATGIGTGTGAGTCATGGCCATCTGATTCATACAGAATTGCC 676

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977 ATACTICCAGAAAACTITGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTCATA 1036
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                                                                        321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle
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                                           677 ITTACTATCTCTTTTATTGCTAGTTCAGTATATTCTGCCCTTAGTTTTGTCTTACTGTAAGT
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immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; receptor. Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina Li F; Zeng H; Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Claim 151; SEQ ID NO 666; 542pp; English Parkinson's disease. 09-SEP-2003; 2003WO-US028226, 09-SEP-2002; 2002US-0409303P, 09-APR-2003; 2003US-0461329P. WPI; 2004-390329/36. N-PSDB; ADO30001. (PRIM-) PRIMAL INC WO20040400000-A2 Homo sapiens. 13-MAY-2004

The invention relates to human and mouse g protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of treating, preventing or diagnosing diseases of the invention; methods of screening for associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; at ransgenic mouse comprising a GPCR gene of the invention; a menuse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polymucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors of probes which hybridise to GPCR polymucleotides of the invention. The invention further discloses variants of the GPCR polympeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acid. Alzheimer's disease.

CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the disponeis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, diseases including neurological disorders (e.g., Alzheimer's disease, disease, disease, food poisoning or irritable bowel candernal gland; disorders (e.g., angina, cardiac arrhythmia or myconders of the adrenal gland; disorders (e.g., angina, cardiac arrhythmia or myconders (e.g., angina, cardiac arrhythmia or myconders of the disorders (e.g., angina, cardiac arrhythmia or angenema or leukaemia); immune disorders (e.g., angina, cardiac arrhythmia or there are disorders of the kidney, liver, lung, breast, overy, anamema or leukaemia); immune disorders (e.g., angina, cardiac arrhythmia or therus, prostate, testis, skin, stomedon, pancreas, spleen, thymus and thyroid (e.g., cancers). The full sequence data for this patent di

Similarity: Percent Similarity: Query Match: DB: US-09-771-956-4 (1-1406) x ADO29564 (1-455)

4 4 0 0 0 0 R R R R Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.34e-253 2385.00 100.00% 100.00% 96.17% Alignment Scores: Pred. No.:

1097 AGAGTAAAACGTTCTGTTACAAGAATAAAAAGAGATCTCGAAGTGTTTTCTACAGACTG 1156

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136 196 256 316 100 376 120 436 140 496 916 977 ATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTTCTTCATCCAGTAAGTTCATA 1036 CCAGGGGTCCCCACTTGCTTTGAGATAAACCTGAAGAAAATTCAGATGTTCATGAATTG 1096 IleLeuileSerileAlaileValArgTyrHisMetileLysHisProlleSerAsnAsn 160 556 919 200 676 220 736 856 280 40 9 300 916 320 80 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn AAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCAGTCTGG 137 GATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTCTGATTGGGCTCTATACATTT 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeulleLeuMetAlaLeuMetLysLysArg 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu TATGGGGAATCTACTTATTTTAATGGCTCTCATGAAAAGCGT GIGCTGTTTTGCTCACCTTTCACACTGACGTCTGTCTTGCTGGATCTTTGGC AAAGTCATGTGCCATATTATGCCTTTTCTTCAATGTGTGTCAGTTTTGGTTTCAACTTTA HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu CTCTCTGGCAGCCATAAATGGAGTTATTCATTCATCAAAAAACACAGAAGAAGATATAGC ProdlyvalProThrCysPheGlu11eLysProGluGluAsnSerAspValH18GluLeu ATTITAATATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT TTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTCTGGACACTAGGTTTTGCCATC LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla PheThrileSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer LeuSerGlySerHisLysTrpSerTyrSerPhelleLysLysHisArgArgArgTyrSer 257 AATCAGAAGACTACGGTAAACTTCCTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTT TGTTCTCCCCTTCCAGTGTTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTCAGCA TTGCTGAGCAGCAGGTATTTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCC CATACAAGTGTCTGCAGAAGTATAAGCTGTGGATTGTCCAACAAAGAAACAGACTTGAA GAAAATGAGATGATCAACTTTAACTCTTCATCCAAAAAAAGAGTGGGCCTCAGGTGAAA 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle **AAGAAGACAGCATGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA** TITACTATCTCTTTATTGCTAGTTCAGTATATTCTGCCCTTAGT GTAAGTCTTCTTGGCTT 77 21 197 317 377 437 141 497 161 557 181 617 201 221 737 677 241 197 281 917 1037 857 301 Dp ठे 셤 ò g ઠે d ò Ω ò q g 8 ò D D ò g õ d δ d ò 셤 à g à g ઠે 엄 ð 엄 음 à ò g

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ACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCATTTGT 1276
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The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that medulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, persoure, locomotors and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPYS receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is african green monkey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein; transmembrane; TM domain; therapy; obesity; blood pressure; eiplepsy; Huntington; & disorder; Parkinson's disorder; eating disorder; seizure; locomotor; anxiety disorder; limbic seizure; tranquilliser;
                                                                    ACCATACTGATATTAGTATTTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTGGTA
                                                                                                                                                                                      CATTIGINGGGCATGATGTCCTGTTGTCTTAATCCAATTCTATATGGGTTTCTTAATAAT
                                                                                                                                                                                                                                                       1337 GGGATTAAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                           African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.
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no acids, useful as targets
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   Length:
Matches:
Conservative:
Mismatches:
Indels:
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CC antagonists could be used to treat obesity and diabetes by reducing CC apperite and food consumption, while agonists could be used to treat CC anorexia XX Sequence 445 AA;	Alignment Scores: Pred, No.: Score: Score: Score: Percent Similarity: Dest Local Similarity: Dest Loc	ATTTAGAGCTCGACGAGTATTAT 	Oy 107 GCCACTCGGAATTCTGATTTCCCAGTCTGGGATGACTATAAAAGCAGTGTAGATGACTTA 16	Qy 167 CAGTATTTCTGATTGGGCTCTAIACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 22	Qy 227 CTTATTTAATGGCTCTCATGAAAAAGCGTAATCAGAAGACTACGGTAAACTTCCTCATA 28	Qy 287 GGCAATCTGGCCTTTTCTGATATCTTGGTTGTGCTGTTTTGCTCACACTGACG 34	347 TCTGTCTTGCTGGATCAGTGGATGTTTGGCAAAGTCATGTGCCATATTATGCCTTTTTCTT	101 ServalbeuLeuAspGInTrpMetPheGlyLysValMetCysHisIleMetF 407 CAAIGTGIGTGAGTTTIGGTTTCAACTTTAATTTTAATATCAATTGCCATTG	121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr	Oy 467 CAFATRAGATRACARTCTRATAATTAACAGCAACCATGGCTACTTCTGATA 52	Qy 527 GCTACTGTCTGGACACTAGGTTTTGCCATTGTTCTCCCCTTCCAGTGTTTCACAGTCTT 58	587 GTGGAACTTTCAAGAAACATTTGGTTCAGCATTGCTGAGCAGGCAG		647 TCAIGGCCAICTGATTCATACAGAATIGCCTITACTATCTCTTTATIGCTAGITCAGIAT	201 SeritpProSerAspSeriyrargileAlaPheinfil 707 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAG	221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArg	Oy 767 GGATTGTCCAACAAAGAAACAGTTGAAGAAATGAGATGATGAACTTGAACTTCTTCAT 824 DD 241 GJYEUSGFASHLYSGLUASAAGJUGUASHGLUAETIAASTLEUThrEEUHis 266	AGT	Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 28	ATGTGTGTTAC
Qy 977 ATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTTCATCCAGTAAGTTCATA 1036 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340 Qy 1037 CCAGGGGTCCCCACTTGGTTTTGAGATAAAACCTGAAGAAATTCAGATGTTCATGAATTG 1096	Db 341 ProGlyvaiProrhrCysPheGluileLysProGluidanSerAspValHisGluiLeu 360 Oy 1097 AGAGTAAAACGTTCTGTTACAAGAATAAAAAGAAGATCTCGAAGTGTTTTCTACAGACTG 1156 Oy 1157 ACATAACTACTAGTTACATTTGTTACATGAACGTCTTTCTACAGACTG 1156 Oy 1157 ACATAACTAATTACTTTTGTTAGTTGCATGCCACTACACCTTTTCCATGTGTA 1216 Db 381 ThrIleLeullaLeuValPhALaValSerTTpMetProLeuHisLeuPhehisValVal 400	Qy 1217 ACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCATTTGT 1276	Oy 1277 CATTIGITGGGCATGATGTCCTGTTGTCTAATCCAATTCTATAGGGTTTCTTAATAAT 1336 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProlleLeuTyrGlyPheLeuAsnAsn 440	Qy 1337 GGGATTAAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381	RESULT 12 AAW27604 1D AAW27604 standard, protein; 445 AA.	AC AAW27604; XX DJ 14-APR-1998 (first entry)	Human neuropeptide Y receptor (NPY Y5).		XX WACATATAGE AT		AX XX D8-APR-1997; 97WO-US005781. PR 08-APR-1996; 96US-0014969P	(FARB) BAYER CORP.	AA PI Hu Y, Mccaleb ML, Bloomquist BT, Flores-Riveros JR, Cornfield LJ; xx	DR WPI, 1997-512637/47. DR N-PSDB; AAT73602.	M. Nucleic acid molecule encoding neuro:peptide Y receptor - useful to PT identify antagonists and agonists, e.g. treat obesity, diabetes, PT hyperlipidaemia and anorexia.	XX PS Claim 2; Page 37-39; 49pp; English.	XXX A novel human receptor for the neurotransmitters neuropeptide Y (NPY) and CC peptide YY (PYY) is designated NPY YS receptor. Its amino acid sequence	was deduced from a human genomic DNA clone (see AAT87940). also been identified (see AAW27602-03). These polypeptides	expressed in host (e.g. human 293) cells. The effects of NPY include blood pressure regulation, memory enhancement, anxiolysis/sedation an increased fond in the contract of t	increased food intake. The receptor can therefore be used to antagonists and agonists capable of controlling these condi-

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Alignment Scores:
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421 AsnProlleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide Y-Y5; appetite; obesity; G-protein coupled receptor; antiobesity; hypotensive; neuronal growth factor; cardiovascular drug; anti-psychotic; neuroleptic; antidiabetic; agonist; antagonist.
                                                           GAAAGACCTTCTCAAGAGAACCACTCCAGAATACTTCCAGAAAACTTTGGCTCTGTAAGA
                                                                                                                                                                    ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArg11eLys
                                                                                                                                                                                                                                                                                                                                   TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn
                                                                                     GluArgProSerdInGluAsnHisSerArglleLeuProGluAsnPheGlySerValArg
                                                                                                                                            AGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATAAAA
                                                                                                                                                                                                                                                                                                           AAGAGATCTCGAAGTGTTTTCTACAGACTGACCATACTGATATTAGTATTTGCTGTTAGT
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designated NPY-Y5 receptor, is a G-protein coupled receptor of NPY, which is involved in appetite/Obesity regulation. Its amino acid sequence was deduced from isolated genomic (AAT66909) and foetaal brain cDNA (AAT66910) sequences. Rat (AAM15232) and mouse (AAM15233) NPY-Y5 receptors have also been identified. NPY-Y5 receptors can be expressed on the cell surface of host (pref. CHO, human embryonic kidney 293 or insect £59) cells. The receptors or host cells can be used to screen for NPY (ant) agonists useful as potential hypotensives, cardiovascular drugs, neuronal growth factors, anti-psychotic, anti-obesity or anti-diabetic drugs
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This sequence represents the human neuropeptide Y5 receptor (Y5) protein. The protein is useful for screening for compounds able to be used as agonists and antagonists to the Y5 receptor, especially for the treatment obesity and diabetes and for developing antibodies for the detection of the protein
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Chimeric mammalian neuropeptide Y5 receptor polypeptides useful for treating a range of disorders including jet lag, hypertension and sexual

N-PSDB; AAZ46232

disfunction.

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                                                                      GAAAGACCTTCTCAAGAACCACTCCAGAATACTTCCAGAAAACTTTGGCTCTGTAAGA 1006
                                                                                                               AGTCAGCTCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCCACTTGCTTTGAGATAAAA 1066
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                                            Neuropeptide Y; NPY; receptor; Y5; G-protein coupled; expression; chimeric; pharmacological property; peripheral nervous system; central nervous system; physiological, activity; food intake; feeding; thermogenesis; blood pressure; hormone release; gut moility; smooth muscle tone; sleep; circadian rhythm; neuronal excitability; nociteption; modiception; anexional response; selzure activity; diuresis; natriuresis; calciuresis; antisenes; agonist; antagonist; obesity; hypertension; epilepsy; sexual dysfunction; jet lag.
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                                                                                   GluargProSerGlnGluAsnHisSerArg1leLeuProGluAsnPheGlySerValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NPY (neuropeptide Y) Y5 receptor.
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This sequence represents human neuropeptide Y (NPY) YS receptor, CDNA encoding which was isolated and amplified from a human neuroblastoma cell encoding which was isolated and amplified from a human neuroblastoma cell line using primers AA464512-6423. The receptor was transiently expressed in COS1 cells, Dit is leave to that of the rat NPY YS receptor. (AAY52579). The invention relates to a chimeric rat/Numan NPY receptor. Comprising the 5' untranslates to a chimeric rat/Numan NPY receptor. Comprising the 5' untranslated region (5' UTR) and extreme 5' coding comprising the 5' untranslated region (5' UTR) and extreme 5' coding comprising the 5' untranslated region (5' UTR) and extreme 5' coding comprising the 5' untranslated region (5' Edebtor, CDNA, When transfected into COS1 cells, the chimeric construct yielded levels of expression higher than the native human YS receptor. The pharmacological properties of the chimeric continer at YS receptor. The pharmacological properties of the chimeric corpus rat YS receptor. The pharmacological properties of the chimeric corpus and similar or greater levels of expression than the chimeric corpus for any wide range of physiological activities including effects on food intake, thermogenesis, blood pressure, hormone release, gut motility, conciented in the feet of and circadian rhythms, neuronal excitability, conciented and encitonal responses. NPY mediates the effects of physiological effects via interactions with at least six distinct Gracian coupled receptors (designated X1.Y6). The YS receptor mediates complexed to receptor, associated nucleic acids (e.g., expression vectors or antisense complexed such as obseity, hypertension, epilepsy, sexual dysfunction and disorders such as obseity, hypertension, epilepsy, sexual dysfunction and cit lag associated with abnormal expression/activity of NPY
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-DEV_BETR_79 -QFWT=fastan -SUFFIX=n2p.mpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DSW_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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A45490
S12863
S12863
B46133
S27388
I39182
G602300
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JC7809
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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neuropeptide Y/peptide YY receptor YI - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Date: 27-0ct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S71152, S55924 S. Wartens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D. R. Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D. R. Reference number: S71152 A;Accession: S71152 A;Accession: S71152 A;Accession: S71152 A;Accession: S7154 A;Accession: S7155 A;Accession: S
                                                                                                                                                                                                                                                                                                                                                     grant of the control 
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A;Molecule type: mRNA
A;Residues: 1-278, T. 280-366 <BLO>
A;Cross-references: EMB::L25416; NID:g409169
C;Superfamily: neuroxinin 1 receptor
C;Reywords: G protein-coupled receptor; transmembrane protein
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TATAACAAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCA 130

Gaps:

US-09-771-956-4 (1-1406) x S71152 (1-366)

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cone (NCBIN:128005, NCBIP:128000)
ss, G.; Shine, J.; Selbie, L.A.
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rbor couples to two different second messenger s
PMID:1321422
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                                                                                                                    ATGACAATCTTATTTCAAATAGGCATTTCAAG 1258
                                                                                                                                                                                                                                                                                                                                                             GCATGATGTCCTGTTGTCTTAATCCAATTCTA 1318
                                                                                                                                                                                                                     alValGlyPheAlaLeuCysTrpLeuProPhe 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selbie, L.A.; Auer, B.; Shine, J.
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Jazin, E.; Yoo, H.; Wahlested, C.
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QQ	2 AsnSerThrLeuPheSerGlnValGluAsnHisSerValHisSerAsnPheSerGluLys 21	ò
ò	116 AATTCTGATTTCCCAGTCTGGGATGACTATAAAAGCAGTGTAGATGACTTACAGTATTT 175	a qu
QQ		2
Š	176 CTGATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTACTTATT 232	G G
QQ	42 ThrLeuAlaLeuAlaTyrGlyAlaVallleIleLeuGlyValSerGlyAsnLeuAlaLeu, 61	ò
ò	233 TTAATGGCTCTCATGAAAAAGCGTAATCAGAAGACTACGGTAAACTTCCTCATAGGCAAT 292	QQ
qu	62 ileileileileuLysGluMetArgAsnValThrAsnIleLeulleValAsn 81	RESULT 3
ζŎ	293 CTGGCCTTTTCTGATATCTTGGTTGTGCTGTTTTGCTCACCTTTCACACTGACGTCTGTC 352	S12863 G protei
qq	82 LeuSerPheSerAspLeuLeuValAlaIleMetCysLeuProPheThrPheValTyrThr 101	C; Specie C; Date:
ò	353 TIGCIGGAICAGIGGAIGTIGGGAAAGICATGIGCCAIATTAIGCCTITICTICAAIGT 412	C;Access R;Eva, C
q	102 LeuMetAspHisTrpValPheGlyGluAlaMetCysLysLeuAsnProPheValGlnCys 121	FEBS Let A; Title:
\$	413 GIGICAGITITGGITTCAACTITAATTITAATATCCATTGCCAITGTCAGGIATCATATG 472	A;Refere A;Access
qq	122 ValSerlieThrValSerllePheSerLeuValLeuileAlaValGluArgHisGlnLeu 141	A;Molecu A;Residu
ò	473 ATAAAACATCCATATCTAATAATTTAACAGCAAACCATGGCTACTTCTGATAGCTACT 532	A; Cross-R; Krause
QC	142 ilelleAsnProArgGlyTrpArgProAsnAsnArgHisAlaTyrValGlyfleAlaVal 161	submitte A;Descri
ò	533 GTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTCTTTCACAGTCTTGTGGAA 592	A;Refere A;Access
qq	162 ileTrpValLeuAlaValAlaSerSerLeuProPheLeuIleTyrGlnValMet 179	A;Molecu A;Residu
λŏ	593 CITCAAGAAACATITGGITCAGCATTGCTGAGCAGCAGGTATITATGTGT 643	A; Cross-C; Superi
qq	180 ThraspdlubropheGlnasnValThrLeuaspalaTyrLysAspLysTyrValCysPhe 199	C; Keywol F;39-61/
λŏ	644 GAGTCATGGCATCTATACAGAATTGCCTTTACTATCTCTTTATTGCTAGTTCAG 703	F;73-93/ F;114-13
Ωp	200 AspGlnPheProSerAspSerHisArgLeuSerTyrThrThrThrLeuLeuValLeuGln 219	F;155-17 F;213-2
δλ	704 TATATICIGCCCTIAGITIGICITACIGIAAGICATACAAGIGICIGCAGAAGIATAAGC 763	F;262-28
дg	220 TyrPheGlyProLeuCysPheIlePheIleCysTyrPheLysIle 234	F;2,11, F;346/B
Ολ	764 TGTGGATTGTCCAACAAAGAAAACAGACTTGAAGAAAATGAGATGATCAACTTAACTCTT 823	Alignme
qq	234 234	Pred. No
ολ	824 CATCCATCCAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTAT 883	Percent Best Loc
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ò	884 TCATTCATCAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTTACCTGCT 943	7-60-80
Dþ	235TyrIleArgLeubysArgArg241	
ò	944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGAATACTTCCAGAAAACTTTGGCTCTGTA 1003	7 6
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70	1004 AGAAGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATA 1063	3 8
Ωp	241 241	· è
ζ	1064 AAACCTGAAGAAATTCAGATGTTCATGAATTGAGAGTAAAACGTTCTGTTACAAGAATA 1123	Q Q

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ein-coupled receptor FC5 - rat

ies: Rattus norvegicus (Norvay rat)
1.12-Fb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
Silon: S12863; S19101
C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
ett. 271, 81-84, 1990
e: Molecular cloning of a novel G protein-coupled receptor that may belong to the resence number: S12863; MuID:91032093; PMID:2172008
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cule type: mRNA
dues: 1-343, 'DNETIAMSTMHTDVSKTSLKQASPVAPKKISMNDNEKI' <KRA>
dues: 1-343, 'DNETIAMSTMHTDVSKTSLKQASPVAPKKISMNDNEKI' <KRA>
dues: 1-343, 'DNETIAMSTMHTDVSKTSLKQASPVAPKKISMNDNEKI' <KRA>
dues: 1-343, 'DNETIAMSTMHTDVSKTSLKQASPVAPKKISMNDNEKI' <KRA>
stemily: neurokinin 1 receptor: glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
11/Domain: transmembrane #status predicted <TM2>
11/Domain: transmembrane #status predicted <TM3>
11/Domain: transmembrane #status predicted <TM3>
11/Domain: transmembrane #status predicted <TM4>
28/Domain: transmembrane #status predicted <TM6>
11/Phinding site: carbohydrate (Asn) (covalent) #status predicted
Minding site: phosphate (Thr) (covalent) #status predicted
Minding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                     1184 AGTICGATACCCACTACACCTITICCATGTGGTAACTGATTTTAATGACAATCTTATTTCA 1243
                                                                                                                                                                                                                                                           1244 AATAGGGATTICAAGIIGGIGIAITIGGAITIGICAITIGIIGGGGAIGAIGICCIGIIGI 1303
                                                 124 AAAAAGAGATCTCGAAGTGTTTTCTACAGACTGACCATACTGATATTAGTATTTGCTGTT 1183
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                                                                                                                                                                                   275 CystrpLeuProLeuThrilePheAsnThrValPheAspTrpAsnHisGlnIleIleAla 294
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------AsnAsnMetMetAspLysMetArgAspAsnLysTyrArgSerSerGlu 257
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0,	57 AsnLeuAlaLeuIleIleIleIleIleIeLeuLysGluMetArgAsnValThrAsnIle 76
281	CTCATAGGCAATCTGGCCTTTTCTGATAT
34	1 CTGACGTCTGTCTTGCTGGATCAGTGGATGTTTGGCAAGTCATGTGCCATATTATG
401	1 TITCTICAATGIGGGGATTIGGTITCAACTITAAITTIAAAATGCCAATIGCCATTGIC 460
46.	AGGTATCATATGATAAAACATCCCATATCTAATAATTTAACAGCAACCATGGCTACTTT 520 :::
521	
581	1 AGTCTTGTGGAACTTCAAGAACATTGGTTCAGCATTGCTGAGCAGCAGG 631
63	2 TATTTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCCTTTACTATCTCTTTA 691
2 69	2 TIGCTAGTICAGTATATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGTCTGC 751
75	2
23	3 233
18	2 AACTTAACTCTTCATCCATCCAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGCAGCCAT 871
23	3 233
872	2 AAATGGAGTTATTCATCAAAAAAAACACAGAAGAAGATATAGCAAGAAGAAGACAGCATGT 931
23	44 YrileArgLeuLysA
932	2 GTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGAATACTTCCAGAAAAC 991
24	6 246
992	2 TTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCAGAAGTTCATACCAGGGGTCCCCACT 1051
1052	TGCTTTGAG
256	6 256
1112	GTTACAAGAATAAAAAAGATCTCGAAGTGTTTTCTACAGACTGACCATACTGATATTA 11
257	ThrLysArgileAsnValMetLeuLeuserileValVal 2
1172	2 GTATTTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTGGTAACTGATTTTAATGAC 1231
1123 0 0	2 AAICTIAITICAAATAGGCATITCAAGITGGIGIATIGCATITGTCATITGTTGTGGGGIG 1291
ת	GINITELIEALAINICYSASNAISASNDEUDEURNELEUDEUCYSAISLEUINIALAMET 30

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erzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
c. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
itle: Cloned human neuropeptide Y receptor couples to two different second messenger & eference number: A46133; MUID:92335184; PMID:1321422
coession: B46133
tatus: preliminary; not compared with conceptual translation
74 AACAAGACACTT-----GCCACAGAGAATAATACTGCT------GCCACTCGGAAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GTAAGTCTTCTTGGCTTTATGGGG 220
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| 117 PheValGInCysValSerIleThrValSerIlePheSerLeuValLeuIleAlaValGlu 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 TCTGATTTCCCAGTCTGGGATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTTCTG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAICTACTTATTTTAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAACTTC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITCTTCAATGTGTGTCAGTTTTGGTTTCAACTTTTAATTTTAATATCAATTGCCATTGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:::: :::||| :::|||
137 ArgHisGlnLeullelleAsnProArgGlyTrpArgProAsnAsnArgHisAlaTyrlle 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 CTGATAGCTACTGTGTGTACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTCAC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AsnSerThrLeuPheSerArgValGluAsnTyrSerValHisTyrAsnValSerGluAsn 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 AlaValilePheThrLeuAlaLeuAlaTyrGlyAlaValileIleLeuGlyValSerGly 56
                                                                                                                                                                                                                                                              ropeptide Y/peptide YY receptor Y1 - mouse
pecies: Mus musculus (house mouse)
ate: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
ccession: B46133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 CTGACGTCTGTCTTGCTGCATCAGTGGATGTTTGGCAAAGTCATGTGCCATATTATGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTATCATATGATAAAACATCCCATATCTAATAATTTAACAGCAAACCATGGCTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ote: sequence extracted from NCBI backbone (NCBIP:108539)
uperfamily: neurokinin 1 receptor
sywords: appetite; G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39-771-956-4 (1-1406) x B46133 (1-382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 ATTGGGCTCTATACATTT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.41e-35
480.00
42.63%
25.85%
19.35%
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t Local Similarity:
ry Match:
                                                                                                         1352 TTA 1354
                                                                                                                                                           330 Leu 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281
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581 AGTCTTGTGGAACTTCAAGAACATTTGGTTCAGCATTGCTGAGCAGC------AGG 631

red. No.: 480.00 Matches: 114 42.86\$ Conservative: 75 est Local Similarity: 25.85\$ Mismatches: 126 uery Match: 19.35\$ Indels: 9 126 127 19.35\$ (1-382) 18: 9 18: 9 19: 1406) x \$27388 (1-382) 19: 1406) x \$27388 (1-382) 10: 1406) x \$27388 (1-382) 10: 1406) x \$27388 (1-382) 10: 1406) x \$27388 (1-382)	TCTGATTTCCCAGTCTGGGATGACT/	179 ATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGG 220 37 AlaValilePheThrLeuAlaLeuAlaTyrGlyAlaValileIleLeuGlyVal8erGly 56 221 AATCTACTTATTAATGGCTCTCATGAAAAAGCGTAATCAGAAGAACTACGGTAAACTTC 280		TATTATGCCT 4 ::: sLeuAsnPro 1	TITCITCAATGIGICAGITITGGITICAACITIAATTITAATATACAATTGCCATIGIC 46	SGINLEWILETIEABNPYCARGGIYTRPAFGPFCABNASNARGHIBALATYFI ACCTACTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTC STRTVALILETTPVALLEWALANAVAAAASErSErLEWPFOPHEVALILETYRG GTGGAACTTTGGTTCAGCATTGGTGAGCA		692 TIGCTAGITCAGIAITTICIGCCCTIAGITIGICTTACTGIAAGICAIACAGIGICTGC 751	233	9 4	932 GIGITACCTGCTCCAGAAAGACCTTCTCAAGAACCACTCCAGAATACTTCCAGAAAAC 991
Pred. Score Perces Best J Query DB: US-09	y do	8 8	i A &	96 & 96	\$ B &	a & a &	90 O	o o o	do oy	S S	OV OD
Db 177 IleLeuThraspGluProPheGlnashvalSerLeuAlaalaPheLysAspLys 194 Qy 632 TATTTATGTGTGATGGCGATCTGATTCATACAGATTGCCTTTACTATTTA 691	AACTTAACTCTTCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGGCAGCCAT 87	Db 233 233 Qy 872 AAATGGAGTTATTCATCAAAAAAACACAGAAGAAGATATAGCAAGAAGAAGATGT 931 Ch 234	932 GIGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGAATACTTCCAGAAAAC 9	Oy 992 TITGGCTCTGTAAGAGTCAGCTCTCTTCATCAGTAAGTTCATACCAGGGGTCCCCACT 1051	SATATTA	Qy 1172 GTATTTGCTGTTAGTTGGATGCCACTACCACTTTCCATGTGGTAACTGATTTTAATGAC 1231	Qy 1292 AIGTCCTGTTGTCTAATCCAATTCTATATGGGTTTCTTAATAATGGGTTTAAAGCTGAT 1351 1::	Db 330 Leu 330 RESULT 5 S27388 SAT388 - mouse	musculus (house n 1997 #sequence_re 7738 rto, A.; Sprengel, rto, A.; Sprengel, rto, NPY-1 recept	A; Reference number: S27388; MUD:93106169; PMID:1468559 A; Accession: S27388 A; Status: preliminary A; Molecule type: DNA	A, residerences: L-36, ZEVA7, A, CONSTRUCTOR A, CROSSTATA, PIDN:CAA79157.1, PID:g53439, C, Superfamily: neurokinin 1 receptor Alignment Scores:

	09 809 ATCAACTTAACTCATCAACAAAAGAGTGGGCCTCAGGTGAAACTCTCGGCAGC 868 247 '31. 249
TTTC TGC1 GTT7 GTT7 Alae GLD1 GDD1 HISS TTA	### ### ##############################

Db 262 262 Qy 989 AACTITGGCICTGTAAGAAGTCAGCTCTCTTCATCCAGTACTACCAGGGTCCCC 1048 Db 262	Oy 1229 GACAATCTTATTTCAAATAGGCATTTCAAGTTGGTCATTTGTTGTTGGGC 1288 Db 292 HisGluAlalleProlleCysHisGlyAsnLeuvlalCysHisLeubeulan 311 Oy 1289 ATGATGTCTGTTGTTAATCCAATTCTATATGGGTTTTTAATAGTGGATTAAAGCT 1348 Db 312 MetalaSeTThrCysValAsnProPheileTyrGlyPheLeuvsnThrAsnPheLysLys 331 Oy 1349 GATTTAGTCCTGTTATT 1366 ::::: Bb 332 GluileLysAlaLeuVal 337 RESULT 8 \$63685 neuropeptide Y receptor D type - mouse C;Species Mus musculus (house mouse) C;Date: 20-Uul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Uul-2004 C;Accession: 863685 C;Caccession: 863685 R;Gergor, P: Milham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J. FEBS Lett. 381, 58-62, 1996 A;Accession: 863685 A;Aitle: Cloning and characterization of a novel receptor to pancreatic polypeptide, a mc A;Reserence number: 863685 A;Accession: 863685 A;Accession: 863686 A;Accession: 863687 A;Accession: 8	Alignment Scores: Pred. Mo.: Pred. Mo.: 458.00 Matches: Conservative: 458.00 Conservative: 458.00 Conservative: 458.00 Conservative: 458.00 Conservative: 458.00 Conservative: 18.47\$ Mismatches: 128 Gaps: 128 US-09-771-956-4 (1-1406) x 863685 (1-375) Qy 161 GACTTACAGTATTTCTGATTGGCTCTATACATTGTAAGTCTTCTTGGCTTTATGGGG 220
Manuel Control of Services of	Oy 221 ARCHAGGATTTCGATTGGGCTCTATACATTTGTAAGTCTTCTGGCTTTATGGGG 220 161 GACTTACAGTATTTCGATTGGGCTCTATACATTTGTAAGTCTTCTGGCTTTATGGG 220 18 ASPValMetValPhelleValThrSeTfyrSetlleGluThrValvalGlyValLeuGly 58 Oy 221 AATCTACTTATTTAATGGCTCTCATAGAAAAGCGTAATGGTAAGCTTC 280 16 S9 AsnLeuCysLeuWetCysValThrValArgGlnLysGluLysAlaAsnValThrAsnLeu 78 Oy 281 CTCATAGGCAATCTGGCTTTTCTGATACTTGGTGTTTTGGTGATTTTGCTCACA 340	581 AGTTTOTGGAACTTCAAGAAACATTTGGTTCAGCATTGCTGAGCAGC [

Qy	401 TITCTICAATGIGIGICAGITITGGITICAACTITAATAITAATATCAATIGCCATIGIC 460 :::	C;Species: Homo sapiens (man) C;Date: 01-Mar-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004 C;Accession: I39187; I39163; \$\overline{G}\$02301 R;Gerald, C.; Walker, M.W.; Vaysse, P.J.
රු දි	461 AGGTATCATATGATAAAACATCCCATATCTAATAATTTAACAGCAAACCATGGCTACTTT 520 	U. Blot. Cnem. 270, 26758-26761, 1995 A/Title: Expression cloning and pharmacological characterization of a human hippocampal r A/Reference number: 139187; MUID:96070760; PMID:7592910 A/Accession: 139187
à i		A.Status: preliminary A.Moolecule type: mRNA A.Residus: 1-381 <ger></ger>
a 8	159 GlylleValValileTrpPheileSerCysPheLeuSerLeuProPheLeualaAsnSer 178 569CQAGTGTTTCACAGTCTTTGGAACTTTCAAGAAAAAAAAAA	A,Cross-references: UNIPROT:P49146; EMBL:U36269; NID:g1063633; PIDN:AAC50281.1; PID:g106388; P.M.; Fernandes, P.; Lymch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kier
역	ThrLeuAsnAspLeuPheHisTyrAsnHisSerLysValValGlu	D. BLOT. CLUENT. 27, 22091-22004, 1995 A.Title: Cloning and functional expression of a CDNA encoding a human type 2 neuropeptide A.Reference number: 139163; MUID:96032678; PMID:7559383
yo,	608 GGTTCAGCATTGCTGAGCAGGTATTTATGTGTTGAGTCATGGCCATCTGATTCATAC 667	A:Accession: 139163 A:Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: mRNA
<i>λ</i> ο :	AGAATTGCCTTTACTATCTTTATTGCTAGTTCAGTATATTCTGCCCTTAGTTTGTTT	A) Testiques: 1-133; A, 135-381 < ROS> A) Cross-references: EMBL: U35500; ND: 91000750; PIDN: AAA93170.1; PID: 91000751 R; Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W. submitted to the EMBL Data Library. December 1995
<u>a</u> 8	211 ArgLeuileTyrThrThrThrPheLeuLeuLeuLeuPheGlnTyrCysIleProLeuAlaPheile 230 728 ACHGHAAGHCATACAACHGHGHACAAAAAGHRAAAAGHGGAHHAAAAAAAAAA	A; Reference number: H01019 A; Accession: G02301
d d		A,3cleculs type: mRNA A,Molecule type: mRNA A,Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <yan></yan>
ò	788 AGACTTGAAGAAAATGAGATGATCAACTTAACTCTTCATCCATC	A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID:g1314330 C;Genetics: Appendix Appe
Q O		A;cene: GDB:NF12K A;cene: GDB:4365607; OMIM:162642 A;Map Dosition: 4031-4031
60 :	848 CAGGIGAAACTCTCTGGCAGCCATAAATGGAGTTATTCATTCATCAAAAAACACAGAAGA 907	C:Superfamily: negration is receptor C:Superfamily: negrit of protein receptor C:Keywords: appetite; G protein-coupled receptor: alvcoprotein: linoprotein: thiolester b
දි දි	241 241 908 AGATATAGGAAGAAGAGAGATGTGTGTTACTTGCTGCAGAAAGACAAGAGAAG 967	
QQ		F;221-237/Domain: transmembrane #status predicted <tms></tms>
ે દે	AGAAGTCAGCTCTCTTCATCCAGT	F;305-328/Onmain: transmembrane #status predicted <tm7> F;302/Dislifide bonds: #status predicted F;342/Binding site: palmitate (Cys) (covalent) #status predicted</tm7>
3 8	n. extantoxtacy social vert Argatacy Gainmer	F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted
<u> </u>	AAGTICATACCAGGGTCCCCACTTGCTTTGAGATAAAACCTGAAGAAATTCAGATGTT	2 Length:
ò	CATGAATTGAGAGTAAAACGTTCTGTTACAAGAATAAAAAAGAGATCTCGAAGTGTTTTC 1	ilarity: 43.03 Similarity: 25.43
qq	261	Indels: Gaps:
ò i	TACAGACTGACCATACTGATATTAGTATTTGCTGTTAGATGGGATGCCACTACACCTTTTC	US-09-771-956-4 (1-1406) x 139187 (1-381)
3 8	48/LeumetinimetvaliniralaPheAlaValLeuIrpLeuFroLeuHisValPhe 284 1208 CATGIGGIAACTGATTITAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGTAT 1267	OY 161 GACTIACAGTATTITCIGATIGGGCTCTATACATTIGTAAGTCTTCTIGGGCTTATGGGG 220 Dy 48 GluyalGludalValienallaTvrvesceriletteitening 1
QC	30	221 AATCTACTTATTTTAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAACTTC
δλ	1268 IGCATTIGICATTIGIGGCATGATGTCCTGTTGTCTTAATCCAATTCTATATGGGTTT 1327	
g ?	snProPhelleTyro	281 CTCATAGGCAATCTGCCCTTTCTGATACTTGGTGTGTGTTTTGCTCACCTTTCACA
;		88 PhelleAlaAsnLeuAlaValAlaAspLeuLeuValAsnThrLeuCysLeuProPheThr
SULT		OY 341 CTGACTCTGTTCTGGGATCAGTGGAAGTCATGTGCCATATATGCCT 400 108 LeuthrTyrThrLeumetGlyGluTrpLysMetGlyProValLeuCysHisLeuValPro 127
neurope N;Alter	neuropeptide Y/peptide YY receptor Y2 - human N;Alternate names: neuropeptide y/peptide YY receptor type 2	Qy 401 TTTCTTCAATGTGTGTGTTTGGTTTCAACTTTAATTTTAATATGCGTTGTC 460

qq	128 TyralaginGlyLeuAlaVaiGinValSerThrileThrLeuThrVallleAlaLeuAsp 147	Biochem.	Biophys. Res. Commun. 209, 606-613, 1995
λ	AGGIATCATATGATAAAACATCCCATATCTAATAATTTAACAGCAAACCATGGCTACTTT	A; Ilcle: A; Refere A; Access	
음 상 음	148 ArgHisArgCysIleValTyrHisDeuGluSerLysIleSerLysArgIleSerPheLeu 167 521 CTGATAGCTACTGTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTT 577 :::	A;Status A;Molecu A;Residu A;Cross- C;Superf	A;Status: preliminary; translated from OB/EMBL/DED A;Molecule type: MRNA A;Residues: 1-730 <res> A;Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528 C;Superfamily: neurokinin 1 receptor</res>
\ \delta \ \	CACAGITTGTGGAACTTCAAGAACATTTGGTTCAGCATTGCTGAGCAGGTAT ::: :: ::: GluTyrSerLeuileGluIlelleProAspPhe	Alignment Pred. No.: Score:	Scores: 5.33e-28 Length: 404.00 Matches:
දු අ	635 TTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCCTTTACTATC 685 202 AlaCysThrGluLysTrpProGlyGluGluLysGerIleTyrGlyThrValTyrSerLeu 221	Percent Best Loc Query Ma DB:	Percent Similarity: 41.078 Conservative: 00 Best Local Similarity: 25.75% Mismatches: 138 Query Match: 16.29% Indels: 116 DB: 1
ò	686 TCTTTATTGCTAGTTCAGTATATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGT 745	US-09-771-956	-4 (1-1406) x I52315 (1-370)
ag o	222 SerSerLeuLeulleLeuTyrValLeuProLeuGlyllelleSerPheSerTyrThrArg 241 746 GTCTGCAARAAGGATGTCCAACAAGAAAACAGACTTGAAGAAAATGAG 805	දුරු දුර	86 GCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCAGTCTGGGATGACTAT 145 ::: ::: :::
⁷ 원		δλ	146 AAAAGCAGTGTAGATGACTTACAGTATTTTCTGATTGGGCTCTATACATTTGTA 199
٥٧	806 ATGATCAACTTAACTCTTCATCCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGC 865	qa	70
QQ	24	ð í	200 AGTCTTCTTGGCGTATTTACTTTTTTAATGGCTCTCATGAAAAGCGTAAT 259
ò	866 AGCCATAAATGGAGTTATTCATTCATGAAAAACACAGAAGAAGATATAGCAAGAAGAGA 925 	ପ୍ର	ValValValGlyLeuValGlyAsnCysLeuLeuValLeuVallleArdaAgvalArgAArg >>
QQ		ò	CAGAAGACTACGGTAAACTTCCTCATAGGCAATCTGGCCTTTTTCTGATATCTTGGTTGTG 31
δλ	926 GCATGTGTGTTACCTGCTCCAGAAAGACCTTCTCAGAGAACCACTCCAGAATACTTCCA 985	ସ୍	LeuHisAsnValThrAsnPheLeuIleGlyAsnLeuAlaLeuSerAspValLeuMetCyS
QQ		À,	CTGTTTTGCTCACCTTTCACACTGACGTCTTGCTGGTCAG106A16111164C 3/
δ	r U	අු	AlaAlaCysValProbeuThrbeuAtaTyrAlakheGiukroArgGiy.rpvalrmeGiy 13
QQ	254	ò	AAAGTCATGTGCCGTATTATGCCTTTTCTTCATGTGTGTG
٥٨	46 CCCACTTGCTTTGAGATAAAACCTGAAGAAAATTCAGATGTTCATGAATTGAGAGTAAAA	යු :	4 9
qq	265	à i	######################################
ζ	AAAAAGAGATCTCGAAGTGTTTTCTACAGACTGACCATACTG	qu (51 IntlewintintileAlavatAsparglyIvalvalbeuvalntsFlobeuvigargargarga
QQ	273	ði i	TTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTGGACACTGGACACTTGGTGGTTTGGTGTGGTTTGTGTGTG
8 8	1166 ATATTAGTATTTGCTGTTAGTTGGATGCCACTACACTTTTCCATGTGGTAACTGAUTTT 1225	8 8	61
3 8	AATGACAATTTCAAATAGGCATTTCAAGTTGGTGTATTGCATTTGTCATTTGTTG	· 43	
: 원	41	ð	617 TIGCTGAGCAGCAGCAGTTTATGTGTTGAGTCATGCCCATCTGATTCATACAGAATT 673
ò	1286 GGCAIGAIGICCIGITGICITAAICCAAITCIAIAIGGGITTCTIAAIAAIGGGAITAAA 1345	ପ୍ର	22
qu	314 AlaMetCysSerThrPheAlaAsnProLeuLeuTyrGlyTrpWetAsnSerAsnTyrArg 333	ð	m ·
λ̈́o	1346 GCTGATTTAGTGTCCCTTATACACTGT 1372	d .	24
ପ୍ରପ	334 LysAlaPheLeuSerAlaPheArgCys 342	ði	
RESULT	10	gg	Seriyi valarig val
G prote C, Speci	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	δ £	794 GAAGAAAATGAGATGATCAACTTAACTCTTCCATCCAAAAAAGAGGGGGCCTGAGGTG 355
C; Dare: C; Acces	on 10-sep-1999 #cext_change 19	5 6	55. ASSCRITTINGGERARASANGGAGTTATTCATTCATCAAAAAACACAGAAGAAGTTAT 913
R,Welch	1, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.	λ	AAAC 1.01666786678618678678678678678678678678678678678678678

Fri Oct 22 09:43:53 2004

	86 GCCACAGAAATAATACTGCTGCCACTCGGAATTCT 121 ::::: : ::::: ::::::::::::::::	2 GATTICCCAGICIGGGAIGACIATA	GlyMetProValTrp	182 GGGCTCTRATTGTAAGTCTTCTTGGGTTTATGGGGAATCTACTTTAATGGCT 241 116 ProSerTyrSerMetlleLeuLeuDealaValLeuGlyAsnLeuLeuVallleSerThr 135		302 TCTGATATCTTGGTTGTTGTTGACTCACTTTCACACTGACGTCTGCTTGCT	362 CAGTGGATGTTTGGCAAAGTCATGTGCCATATTATGCCTTTTCTTCAATGTGTGTT 421	422 TTGGTTTCAACTTTAAATTTTAAATTGCCATTGCCATTGTCATATGATAAAACAT 481 	482 CCCATATCTAATAATTTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTC 535	536 TGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTCACAGTCTTGTGGAACTT 595	596 CAAGAAACATTTGGTTCAGCATTGCTGAGCAGCAGGTATTTATGTGTTGAG 646 ::: 255TATTTATGGTTGAG 646	TCAIGGCCAICIGATICAIACAGAATIGCCTITACTAICTCTTTATIGCTAGTICAGTAT 70 PheTipProAspGlnGlyTyrGluLeuPheTyrAsnileLeuLeuAspPheLeuLeuLeu 28	707 ATTCTGCCCTTAGTTTGTCTGTAAGTCATACAAGTGTCTGCAGAAGTATAAAGCTGT 766 ::: :::	767 GGATTGTCCAACAAAGAAACAGACTTGAACAAAATGAGATGAG	CATCCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTAT 88	AladiyGlySerAlaProAsnProGlyThr 33	884 TCATTCATCAAAAACACAGAAGATATAGGAAGAGAGAGAG	CCTGCTCCAGAAAGACCTTCTCAAGAACCACTCCAGAATACTTCCAGAA 98	46 ThrAlaThrAlaValTyrAsnGluAsnSerAsnAsnAsnAsnGlyAsnSerGluGlySer	989 AACTITGGGTCTGTAAGAAGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCC 1048	44, 02
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	Oy 914 AGCAAGAAGACAGCATGTGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCC 973 ::: :::	TAAGTTC	270 Arg	OY 1034 ATACCAGGGGTCCCACTTGCTTTGAGATAAACCTGAAGAAATTCAGATGTTCATGAA 1093 Db 270 270	OY 1094 TTGAGAGTAAAAGGTTCTGTTACAAGAATAAAAAAGAGATCTCGAAGTGTTTTCTACAGA 1153 Db 271	Qy 1154 CTGACCATACTGATATTTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTG 1213 ::::::::: ::	Qy 1214 GTAACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTATTGCATT 1273	Qy 1274 TGTCATTTGTTGGGCATGATGTCCTGTTGTCTTAATCCAATTCTATATGGGTTTCTTAAT 1333	Qy 1334 AATGGGATTAAAGCTGATTTAGTGTCCCTTATA 1366 1340 AspSerPheArgGluLeuArgLysMetLeu 350	RESULT 11 UC7809 sulfakinin receptor protein, DSK-R1 - fruit fly (Drosophila melanogaster)	C;Spectes: Drosophila melanogaster C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004 C;Accession: JC7809 R:Kubiak, T M:: Jarsen M.J: Rurton, K.J. Bannow, C.B. Marrin, R.B. Zantello, M.B.	rosophila melanogaster sul	A;Molecule type: mRNA A;Residues: 1-584 «KUB» A;Cross-references: UNIPROT:Q7M3J6; GB:AX128640 C;Comment: This receptor, the first functionally active orphan Drosophila sulfakinin G-g	nctions. C;Genetics: A;Gene: dsk-rl A.war noeirion: 17	Fils 139/Domain: transmembrane region #status predicted <twr1> Fils-139/Domain: transmembrane region #status predicted <twr2> Fils0.167/Domain: transmembrane region #status predicted <twr2></twr2></twr2></twr1>	r.1097-60/DOMAIN: Latalsmembrane region #status predicted <tmr4> F;229-250/Domain: transmembrane region #status predicted <tmr4> F;275-300/Domain: transmembrane region #status predicted <tmr5></tmr5></tmr4></tmr4>	F;431-454/Domain: transmembrane region #status predicted <tmr6> F;467-491/Domain: transmembrane region #status predicted <tmr7></tmr7></tmr6>	t Scores: 3.35e-26 Length:	Percent Similarity: 41.15% Conservative: 81 Best Local Similarity: 24.49% Mismatches: 186	15.48% Indels: 2 Gaps:	US-09-771-956-4 (1-1406) x JC7809 (1-584) QY 35 CAGGACTATAATATGGATTTAGAGCTCGACGAGTATTATAACAAGACACTT 85

323 TTTTGCTCACCTTTCACACTGACGTCTTGCTGGATCAGTGGATGTTTGGCAAAGTC 382		209 TrpGlnThrPheLeuLeuLleuLeuris::::::::::::::::::::::::::::::::::::	AGATATAGCAAGAAGACAGCTGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACACTTCTCAAGAGAACACTTCTCAAGAGAACACTTCTCAAGAGAACACTTCTCAAGAGAACACTTCTCAAGAGAACACTTCTCAAGAGAACACTTTGGTTTTTGGTTCTTTAAGAAGTTCAGCTCTTCTTCATCCAGTCAGCTCTCTTCATCAAGAAACTTTGGCTCTGTAAGAAGTCAGCTCTTCTTCATCCAGTACACTCTCATCATCAGTAGAAGTTAGGTTCATCATCATCAGTAGTAGAAAGTTAGGCTCTCTTCATCATCAGTAGTAGAAAGTTAGGCTCTCTTCATCATCCAGTAGTAGAAAACTTTGGCTCTGTAAGAAGTCAGTTGTAAGAAGTTCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	1028 AAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATAAAACCTGAAGAAATTCAGATGTT 1087 297SerGlyGlyArgile 301 1088 CATGAATTGAGATAAAAGAGAATAAAAAAAGAGATCTCGAAGTGTTTTC 1147 302 AshArgileArgSerSerGlySerAlaAlaAshLeulleAlaLysArgValile 320	1148 TACAGACTCACCATACTATAGTATTTGCTGTTAGTTGGATGCCACTACACCTTTTC 1207 321 ArgMetLeu1leValileValvalLeuPhebheieuCygTrpMetProllePheSerala 340 1208 CATGTGGTAACTGATTTTAATGACAATCTTATTTCAAATAGGCATTCAAG 1258 121 AsnAlaTrpArgAlaTyrAspThrValSerAlaGlubysHisLeuSerGlyThrPro 359 1259 TTGGTGTATTGCATTTGTTGGCATGATGTCCTTTAATCCAATTCTA 1318 1259 TTGGTGTATTGCATTTGTTGGCATGATGTCCTTTAATCCAATTCTA 1318 126
8 6 8 6 8 6 8	8 8 8 8	4 8 8 8 8 8		3 8 8 8	Oy Oy Oy Oy Oy Oy Oy RESULT
Db 386 ThrValileThrThrThrThrThrThrThrLeuAlaLysThrSerSerProSer 405 Qy 1079 TCACATGTTCATGAATTGAGAGTAAAACGTTCTGTTACAAGAATAAAA 1126 Db 406 IleArgValHisAspAlaAlaLeuArgArgSerAsnGluAlaLysThrLeuGluSerLys 425 Qy 1127 AAGAGATCTCGAAGTGTTTCTACAGACTGACTGATATTAGTATTTGTGTTTAGT 1186 Db 426 LyeArgValvalLysMetLeuPheValLeuGluPhePheIsCys 442 Qy 1187 TGGATGCCACTACCCTTTTCCAT	463 TyrvalAspTyrThralaileSer	RESULT 12 JGS599 cholecystokinin-A receptor - mouse C;Speciase: Mus musculus (house mouse) C;Speciase: Mus musculus (house mouse) C;Accession: 075599 K;Lacourse, K.A.; Lay, J.M.; Swanberg, L.J.; Jenkins, C.; Samuelson, L.C. B;Ochem. Biophys. Res. Commun. 236, 630-635, 1997 A;Title: Molecular structure of the mouse CCK-A receptor gene. A;Reference number: JCS599; MUID:97396148; PMID:9245702 A;Accession: JC5599 A;Status: nucleic acid sequence not shown	A,Molecule type: DNA A,Residues: 1-436 <lac> A,Residues: 1-436 <lac> A,Cross-references: UNIPROT:008786 A,Cross-references: UNIPROT:008786 A,Note: translation not complete C;Comment: This receptor belongs to the seven transmembrane G-protein coupled receptor fider contraction, and cholecystokinin inhibition of food intake. C;Superfamily: neurokinin 1 receptor F;42-67/Domain: transmembrane #status predicted <tmm></tmm></lac></lac>	gnment Scores: 1.4e-25 4. No.: 377.00 cent Similarity: 44.06* t Local Similarity: 24.89\$ ry Match: 2.08	US-09-771-956-4 (1-1406) x JC5599 (1-436) QY 83 CTTGCCACAGAGAATAATACTGCTGCCACTCCGAATTCTGATTTCCCAGTCTGGGATGAC 142

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gastric CCK-A receptor - rabbit (Gomestic rabbit)
C)species: Oryccolagus cuniculus (domestic rabbit)
C)species: Oryccolagus cuniculus (domestic rabbit)
C)Accession: S50150
R)Reuben, M., Rishigh, L., Prinz, C.; Hersey, S.; Sachs, G.
B)cochim. Biophys: Acta 1219, 321-327, 1994
A)Title: Cloning and expression of the rabbit gastric CCK-A receptor.
A)Reference number: S50150; MUID:95002144; PMID:7918628
A)Accession: S50150
A)Status: preliminary
A)Andlecule type: mRNA
A)Accession: S10150
C)Superfamily: neurokinin 1 receptor
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|LeuTyrSerLeuIlePheLeuLeuSerValLeuGlyAsnThrLeuValIleThrValLeu
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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43.81%
25.74%
15.12%
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expression of the cholecystokini
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A;Molecule type: protein
A;Residues: 366-389 «Man»
C;Comer: This G-protein-coupled receptor is present in the gastrointestinal system, vac
; smooth muscle contraction of the gallbladder and stomach. It is capable of activating I
ducing the subsequent release of intracellular calcium.
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A.Cross-references: UNIPROT:P30551; GB:M88096; NID:g203383; PIDN:AAA40899.1; PID:g203384
A.Cross-references: UNIPROT:P30551; GB:M88096; NID:g203383; PIDN:AAA40899.1; PID:g203384
A.Reperimental source: pancreas
A.Rote: sequence extracted from NCBI backbone (NCBIN:93814, NCBIP:93815)
R.Taxata, Y., Takiguchi, S., Funakoshi, A.; Kono, A.
B.iochem. Biophys. Res. Commun. 213, 958-966, 1995
A.Title: Gene structure of rat cholecystokinin type-A receptor.
A.Reference number: JC4225.
A.Accession: JC4225.
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R;Mantamadiotis, T.; Baldwin, G.S.
Bacchem. Biophys. Res. Commun. 201, 1382-1389, 1994
A;Title: The seventh transmembrane domain of gastrin/CCK receptors contributes to
A;Reference number: PC2213; MUID:94296413; PMID:8024583
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A;Title: Purification, molecular cloning, and functional expression of the chol A;Reference number: A42685; MUID:92212981; PMID:1313582
A;Accession: A42685
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                                    -----SerSerAlaAlaAlaLeuMetAlaLysLysArgValIleArg
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C;Speciae: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change
C;Accession: A42685; UC4225; PC2213
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C;Genetics:
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A;Introns: 53/1; 137/1; 224/2; 267/1
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C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
F;57-82.Domain: transmembrane #status predicted <TM1>
F;93-119/Domain: transmembrane #status predicted <TM2>
F;131-151/Domain: transmembrane #status predicted <TM4>
F;173-193/Domain: transmembrane #status predicted <TM5>
F;225-249/Domain: transmembrane #status predicted <TM5>
F;330-348/Domain: transmembrane #status predicted <TM5>
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П	Db 270		SerThrArgTyr 278	ω
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н	Db 279		GluAspSerAspGlyCysTyrLeuGlnLysSerArgProProArgLysLeuGluLeuGln 298	œ
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	Qy 1094		AAAAAGAGATCTCGAAGTGTTTTCTACAGA 11	53
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_	370 ad		8	7
	Oy 1325 Db 388	THICTHATAATGGGATTAAAGCTGATTTAGTGTCCCTTATACACTGT ::: :::	<pre>ITAGIGICCCTTATACACTGT 1372 :::::: </pre>	
,	RESULT 15 A41738 neuropeptide	Y receptor - fruit fly (Drose	phila melanogaster)	
	N;Alternate n C;Species: Dr C;Date: 16-Se	NyALTERTATE names: v protein-coupled receptor Fra C.Species: Droscophia melanogaster C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_chan	Sep-1992 #text_change 09-Jul-2004	
	C, Accession: R; Li, X.J.; W	A41738 'u, Y.N.; North, R.A.; Forte, ' 267 9-12 1992	Ä.	
	A;Reference n	ding, functional expression, umber: A41738; MUID:92112730	gulation of a	neuropeptide)
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GGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTACTTATTTAATG 238	CTGGATCAGTGGATGTTTGCCAAAGTCATGTGCCATATTGTTCTTCAATGTGTG 415 ::: ::: LeuAsnTyrTrpProPhedlyLeuAlaLeuCysHisPheValAsnTyrSerGlnAlaVal 173 TCAGTTTTGGTTTCAACTTTAATATTAATATCAATTGCCATTGTCAGGTATCATAGATA 475	23 23 24 24 24	AGCAGGIATTATGTGTTGAGTCATGGCCATCTGATTGCAGAATTGCCTTTACTATC 685LysTyrlle(ATGATCAACTTAACTCTTCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGC 865	GABAACTTTGGCTCTGTAAGAAGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTC 1045
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TISSUE-Hippocampus;
MEDLINE=9631789; bubMed=8700207;
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Batzl-Hartmann C., Smith K.E., Vaysse P., Durkin M.M., Laz T.M.,
Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,
Taber R.I., Branchek T.A., Weinshank R.L.;
Ma receptor subtype involved in neuropeptide-Y-induced food intake.";
Nature 382:168-171(1996).
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MEDLINE-97312686; PubMed-9169127;
Herzog H., Darby K., Ball H., Hort Y., Beck-Sickinger A., Shine J.;
"Overlapping gene structure of the human neuropeptide Y receptor
subtypes Y1 and Y5 suggests coordinate transcriptional regulation.";
Genomics 41:315-319(1997):
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=6421636; PubMed=8824284;
Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,
Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,
Sadlowski Y., Schaefer J., Velazquez N., McCaleb M.L.;
"Identification of a novel hypothalamic neuropeptide Y receptor
associated with feeding behavior.";
J. Biol. Chem. 271:26315-26319(1996).
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01-NVV-1997 (Rel. 35, Created)
05-JVV-2004 (Rel. 35, Last sequence update)
05-JVV-2004 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPYS-R) (NPY-YS receptor)
receptor) (NPYYS).
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NCBI_TaxID=9606;
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(c) 1993 - 2004 Compugen Ltd.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cytoplasmic (Potential).
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PRINTS; PR00237; GPROTEIN RECEP F1 1; FALSE_NEG.

PROSITE; PS00237; GPROTEIN RECEP F1 1; FALSE_NEG.

G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane.
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                       107 GCCACTCGGAATTCTGATTTCCCAGTCTGGGATGACTATAAAAGCAGTGTAGATGACTTA
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MEDLINE-2388257; PubMed=12477932;

MEDLINE-2388257; PubMed=12477932;

MISCALL S., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhart N.K.,

Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhart N.K.,

Appleton M., Soarse M.B., Bonaldo, M.F., Carninci P., Franger A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Will T.B., Toobhyuki S., Carninci P., Prange C.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Minting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
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                                                                              ThrileLeuileLeuvalPheAlaValSerTrpMetProLeuHisLeuPheHisValVal
                                                                                                                                               ACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCATTTGT
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02-MAR-2004 (TTENBIrel. 27, Created)
02-MAR-2004 (TTENBIrel. 27, Last sequence update)
02-MAR-2004 (TTENBILEI. 27, Last annotation update)
02-MAR-2004 (TTENBILEI. 27, Last annotation update)
Neuropeptide Y receptor Y5.
Neuropeptide Y receptor Y5.
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primata; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC042416, AAH42416.1; -.
Neuropeptide; Receptor.
SEQUENCE 445 AA; 50726 MW; A2B0F3169DBA66BE CRC64;
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ad. Sci. U.S.A. 99:16899-16903(2002)
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21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40 167 CAGTATTTTCGATTGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226 11	407 CAATGTGTGTCAGTTTTGGTTTCAACTTTAATTTTAATATGCCATTGTCAGGTAT 466 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140 467 CATATGATAAAACATCCCATATCTAATAATTTAAACACCAAACCATGGCTACTTCTGATA 526 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaasnHisGlyTyrPheLeuIle 160 527 GCTACTGTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTCACAGTCTT 586 161 AlaThrValTrpThrLeuGlyPheAlaIleClySerFroLeuProValPheHisSerLeu 180 587 GTGGAACTTCAAGAAACATTTGGTTCAGCATTGTGAGGGTATTTATGTTGTTGAG 646 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200 647 TCATGGCCATCTGATTCATAAGAAATTGCCTTTAATTGCTAGTTCAGTAT 706 11	707 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAGTGTCTGCAGAAGTATAAGCTGT 766 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240 767 GGATTGTCCAACAAGAAACAGACTTGAAGAAATGAGTGATCAACTTAACTCTCTA 826 241 GlyLeuSerAanLysGluAsnARGLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260 827 CCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGCAGCCATAATTCAT 826 261 ProSerArgLysIleGlyProGInValLysLeuSerGlySerHisLysTrySerTyrSer 280 887 TTCATCAAAAAACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTTACCTGCTCCA 946 887 TTCATCAAAAAACAGAAGAAGATATAGCAAGAAGAAGACTGTGTGTTACCTGCTCCA 946 887 TTCATCAAAAAAACAGAAGAAGATATAGCAAGAAGACATGTGTGTTACCTGCTCCA 946 887 TTCATCAAAAAAACACAGAAGAAGATATAGCATGTGTGTTACCTGCTCCA 946 947 GAAAGACCTTCTCAAGAAGAACCACTCCAGAATACTTTGGCTTTAGCTTCTGTAAGA 1006 947 GAAAGACCTTCTCAAGAAACCACTCCAGAATACTTTCCAGAAAACTTTGGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAAGAAACCACTCCAGAAAACTTTCCAGAAAACTTTGGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAAGAAACCACTCCAGAAAACTTTCCAGAAAACTTTGGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAAGAAACCACTCCAGAAAACTTTCCAGAAAACTTTGGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAAGAAACTACCAGAAAACTTTGGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAAGAAACCATCCAGAAAACTTCCAGAAAACTTTGGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAACAAACTACCAGAAAACTTCCAGAAAACTTTAGCTCTGTAAGA 1006 947 GAAAGACCTTCTCAACAAACTACCAGAAAACTACCAGAAAACTACAGAAAACTACCAGAAAACTACAGAAAACTACAGAAAACTACAGAAAACTACAGAAAACTACAGAAAACTACAGAAAACTACAGAAAACTACAGAAAACTACAGAAAAACTACAAAAACTACCAGAAAAACTACAGAAAAAAAA	AGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATAAAA 10 SerGlnLeuSerSerSerLysPheileProGlyvalProThrCysPheGluileLys 34 CCTGAAGAAATTCAGATGAATTGAGAGAGAGAGAAAAAA 11 [
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	441 HisCysLeuRisMet 445 SULT 3 QSGK73 QSGK73 OL-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Neuropeptide Y receptor Y5. Macaca mulatta (Rhesus macaque). Eukaryota; Metacaa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cararrhini; Cercopithecidae; Cercopithecinae; Macaca. NCBI TaxID=9544; [1] SEQUENCE FROM N.A. MEDLINE=21184974; PubMed=11287088; MEDLINE=21184974; PubMed=11287088; Gackenheimer S., Johnson D., Beavers L.S., Gadski R.A., Baez M.;	4	Alignment Scores: Pred. No.: 2318.00 Matches: Conservative: 445 Secret Similarity: 99.78% Percent Similarity: 99.78% Best Local Similarity: 99.73% Mismatches: 1 Query Match: 2 Best Local Similarity: 99.73% Diagratic Similarity: 99.78% Mismatches: 1 Gaps: 0 Gaps: 0 A7 ATGGATTTAGAGGTGACTGACGAGGAATAATACTGCT 106 A7 ATGGATTTAGAGCTCGACGAGTATTATAACAAGACACTTGCCACAGAGAATAATACTGCT 106 Db

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Lunchell I., Eriksson H., Marklund U., Larhammar D.;

Loppides 22:357-363 (2001)

EMBL; AR536240; AAK52800.1; -

EMBL; AR536240; AAK52800.1; -

GO; GO:0004893; Fireceptor activity; IEA.

GO; GO:0004893; Fireceptor activity; IEA.

GO; GO:0001884; Fireceptor activity; IEA.

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NPY receptor 5.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Hy
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                                                                                                                                                                                                                                                                                                                                                                                                                                         species homologs.";

Regul. Peptr. 75:45-53(1998).

-!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Highest to tachykinins receptors.
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[Votential).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPYS).
Name-NPYSR; Synonyms-NPY5;
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canis.
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99017379; PubMed=9802393; Borowsky B., Walker M.W., Bard U., Weinshank R.L., Laz T.M., VaySse P., Branchek T.A., Gerald C., "Molecular biology and pharmacology of multiple NPY Y5 receptor
                                                                                                                 446 AA
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442
446 AA;
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SEQUENCE FROM N.A.
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Conservative: Mismatches: Length: Matches:

Indels:

Gaps:

286

180 646 200 206 220 166 240

586

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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associated with feeding behavior.";
J. Biol. Chem. 271:26315-26319 (1996).

I. Biol. Chem. 271:26315-26319 (1996).

I. FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders.

I. SUBCELLULAR LOCATION: Integral membrane protein.

I. TASUE SEPECTICITY: Brain, hypothalamus.

I. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

Highest to tachykinins receptors.
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7 (Potential).
Cytoplasmic (Potential).
By similarity.
S-palmitoyl cysteine (Potential).
N-linked (GloNAc. . ) (Potential).
N-linked (GloNAc. . ) (Potential).
W, 5157ABE341BA707E CRC64;
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InterPro; IPR001276; GPCR_Rhodpsn.
InterPro; IPR000137; NPY_receptor.
InterPro; IPR000611; NPY_receptor.
InterPro; IPR000611; NPY_receptor.
Pfam; PF000001; 7tm 1; 1.
PR01037; GPCRRHODPSN.
PROSITE; PS00237; GPCRHODPSN.
PROSITE; PS00227; GPROTEIN_RECEP_F1 1; FALSE_NEG.
PROSITE; PS00262; GPROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
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2 (Potential).
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EMBL; AF044264; AAC15670.1; -
EMBL; U66274; AAC52845.1; -.
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    301 AlaArgProProGlnGluAsnHisSerArgMetLeuProGluAsnPheGlySerValArg 320
                                                                          SerGlnHisSerSerSerSerLysPhelleProGlyValProThrCysPheGluValLys
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Gerald C., Walker M.W., Crisotione L., Gustafson B.L.,
Batzl-Hartmann C., Smith K.E., Vayese P., Durkin M.M., Laz T.M.,
Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,
Taber R.L., Branchek T.A., Weinshank R.L.,
"A receptor subtype involved in neuropeptide-Y-induced food intake.";
Nature 382:168-171(1996).
                                                AGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATAAAA
                                                                                                                                                                                                                                                                                                            TGGATGCCACTACACCTTTTCCATGTGGTAACTGATTTTAATGACAATCTTATTTCAAAT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-98332165; PubMed-9669502;
Parker E.M., Babij C.K., Balasubramaniam A., Burrier R.E., Guzzi M., Hamud F., Mukhopedhyay G., Rudinski M.S., Tao Z., Tice M., Xia L., "Mullins D.E., Salisbury B.G.;
"GR231118 (1229091) and other analogues of the C-terminus of neuropeptide Y are potent neuropeptide Y are potent neuropeptide Y is receptor agonists.";
Eur. J. Pharmacol. 349:97-105(1998).
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MEDLINE=96421636; PubMed=8824284;
Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,
Hu Y., Elcomquist B.T., Cornfield L.J., Decarr L.B.,
Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,
Sadlowski Y., Schaefer J., Velazquez N., McCaleb M.L.,
"Identification of a novel hypothalamic neuropeptide Y receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYSR RAT STANDARD; PRT; 456 AA.
Q63634; P70586;
01-NOV-1997 (Rel. 35, Created)
01-NOV-2097 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPYS-R) (NPY-Y5 receptor) (Y5
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Name=Npy5r; Synonyms=Npy5;
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                             68 MetGlyAsnLeuLeulleLeuMetAlaValMetLysLysArgAsnGlnLysThrYal
                                                                                               TTCACACTGACGTCTGTCTTGCTGGATCAGTGGATGTTTGGCAAAGTCATGTGCCATATT
                                                                                                                                      AIGCCTITITCTICAAIGIGIGICAGITITIGGITITCAACTITIAAITITAAIAITGCC
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                                                  MEDLINE=94859646; PubMed=9315606; DOI=10.1016/S0005-2736(97)00131-4; Nakamura M., Yokoyama M., Watanabe H., Matsumcto T.; Nakamura M., Yokoyama M., Watanabe H., Matsumcto T.; Natsumcto T.; Moining, organization and localization of the gene for the mouse neuropeptide Y-Y5 receptor."; Biochim. Biophys. Acta 1328:83-89(1997).
-!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).
-!- SUBCELULIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- Highest to tachykinins receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] -
SEQUENCE FROM N.A.
MEDLINE=99017779; Pubmed=9802393;
BOLOWSKY B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,
BOLOWSKY B., Branchek T.A., Gerald C.;
"Molecular biology and pharmacology of multiple NPY Y5 receptor
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EMBL; AF022948; AAB1829.1; -.
EMBL; AF022948; AAB1829.1; -.
EMBL; AF001346; BAA8938.1; -.
GD; AG0114608; MAY95r.
GO; GO:001602; C:membrane; IDA.
GO; GO:0001602; F:pencreatic polypeptide receptor activity; IDA.
GO; GO:0001602; F:peptide YY receptor activity; IDA.
GO; GO:0001273; P:regulation of synapse; IMP.
InterPro; IPR000376; GPCR Rhodpsn.
InterPro; IPR000393; NPY5_receptor.
InterPro; IPR000611; NPY_receptor.
FFGML; PF000011; 7tm_1; 1.
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070342; 035380; Q9JMX1;
15-DEC-1998 (Rel. 37, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor)
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
4-APR-2004 (TrEMBLrel. 27, Last annotation update)
11-APR-2004 (TrEMBLRel. 27, Last ann
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     PRINTS; PR00237; GPRCRHODOPSN.

PROSITE; PS00237; G_PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Lipoprotein; Pall G-protein coupled receptor; Glycoprotein; Lipoprotein; Pall Bhosphorylation; Transmembrane.

DOWAIN 1 1 (Potential).

TRANSMEM 96 116 2 (Potential).

DOWAIN 137 158 Cytoplasmic (Potential).

TRANSMEM 137 158 3 (Potential).

TRANSMEM 137 158 Cytoplasmic (Potential).

TRANSMEM 139 199 4 (Potential).

TRANSMEM 232 253 (Potential).

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TRANSMEM 32 448 Cytoplasmic (Potential).

TRANSMEM 32 54 388 Cytoplasmic (Potential).

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Adachi J. Aizawa K. Akimura T. Arakawa T. Bono H., Carninci P.,
Adachi J. Aizawa K. Akimura T. Arakawa T. Bono H., Carninci P.,
A Hayashida K., Hayatsu M., Hiramoto K., Hiracka T., Hirozane T.,
A Hori F., Inctani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Myazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,
Saito H., Saitoh H., Sakai C., Sakzuwe N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takaku-Akahira S., Takeda Y., Tagami M.,
Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/64J IISSUE=Corpora quadrigemina;
MEDIAINE=20499374; PubWed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=22354683; PubMed=12466831;
The FANTOM Consortium,
The FANTOM Genome Exploration Research Group Phase I & II Team;
Thanlysis of the mouse transcriptome based on functional annotation of 60, 770 full-length cDNAs.";
Nature 420:563-573(2002).
                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
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STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=21085660; PubMed=11217851;
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MEDLINE-9927253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
Hitgh-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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musculus (Mouse)
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                                                                                                                                               1064 AAACCIGAAGAAATICAGAIGITCAIGAATIGAGAGIAAAACGITCIGITACAAGAAIA 1123
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1004 AGAAGTCAGCTCTTCATCCAGTAAGTTCATACCAAGGGTCCCCACTTGCTTTGAGATA 1063
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                                        440 LeuAsnProlleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeu 459
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STRAIN=LWD; TISSUB=Kidney;
Ito Y., Minezawa M.;
Submitted Gor-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Receptor for neuropeptide Y and peptide Y. The activity of this receptor for neuropeptide Y and peptide Y. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Highest to tachykinins receptors.
                                                                                                                                                                                                                                                                                                  1124 AAAAAGAGATCTCGAAGTGTTTTCTACAGACTGACGATACTGATATTAGTATTTGCTGTT
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Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P.,
Andersson L., Larhaumar D.;
"Porcine NPY receptors, NPYIR, NPY2R and NPY5R: cloning, mapping and
comparative analysis.";
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuropeptide Y receptor type 5 (NPYS-R) (NPY-YS receptor) (YS
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Sus scrofa (Pig)
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EMBL; AF106083; AAD13778.1; -.

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          InterPro; IPR00276; GPCR. Rhodpsn.
InterPro; IPR000376; GPCR. Rhodpsn.
InterPro; IPR000393; NPY5_receptor.
InterPro; IPR00011; NPY_receptor.
Pfam; PF00001; 7tm 1; NPY_receptor.
PRINTS; PF00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS002262; G PROTEIN RECEP_F1_2; 1.
G_Protein, coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                               7 (Potential).
Cytoplasmic (Potential).
N-linked (GlCNAC. .) (Potential).
N-linked (GlCNAC. .) (Potential).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
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Extracellular (Potential).
Extracellular (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
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Extracellular (Potential).
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Matches:
Conservative:
Mismatches:
Indels:
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080FM3;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide Y receptor Y5.
01-JUN-2003 (TremBlarel. 24, Last annotation update)
Neuropeptide Y receptor Y5.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Robinse; NCBI_TaxID=9031;
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"Pharmacological characterization of cloned chicken neuropeptide y
"receptors YI and YS.";

"I secoptors YI and YS.";

"I whereological characterization of cloned chicken neuropeptide y
"I wencohem. 0.0-0(2003).

"Bebl; AY040844; AAK83556.1;

"R GO; GO:001604983; F:integral to membrane; IEA.

"By GO; GO:00164983; F:integral to membrane; IEA.

"GO; GO:00164983; F:integral to membrane; IEA.

"GO; GO:001884; F:integral to membrane; IEA.

"GO; GO:0004983; F:integral to membrane; IEA.

"GO; GO:0001898; F:integral to membrane; IEA.

"GO; GO:000189; F:integral to membrane; IEA.

"A GO; GO:0000189; F:integral to membrane; IEA.

"A GO; GO:000189; F:integral to membrane; IEA.

"A GO; GO:000189; F:integral to membrane; IEA.

"A GO; GO:000189; F:integral to membrane; IEA.

"A GO; GO:0000189; F:integral to membrane; IEA.

"A GO; GO:000189; F:integral
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MEDILINE=3943/1831

RAY MEDILINE=3943/1831

RAY Starback P., Lundell I., Fredrikason R., Berglund M.M., Yan Y.L.,

RAY Starback P., Lundell I., Predrikason R., Berglund M.M., Yan Y.L.,

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RT Manusopelide Y receptor subtype with unique properties cloned in the representation of the properties of the properties of the receptor "."

REAGINE, MOI Brain Res. 70:242-252(1999).

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RO; GO:0016021; C:integral to membrane; IEA.

RO; GO:0016021; C:integral to membrane; IEA.

RO; GO:0004872; F:neuropeltide Y. receptor activity; IEA.

RO; GO:0001584; F:neuropeltide Y. receptor activity; IEA.

RO; GO:0001584; F:neuropeltide Signaling pathway; IEA.

RO; GO:0001584; F:neuropeltide signaling pathway; IEA.

RO; GO:0001584; F:neuropeltide signaling pathway; IEA.

RO; GO:0001218; P:neuropeltide signaling pathway; IEA.

RITHERPIC: IPRO00351; NPYI_receptor.

RITHERPIC: IPRO0031; Teceptor.

REAM: PRO01218; NREPETIDEYIR.

RRINTS; PRO1013; NREPETIDEYIR.

RRINTS; PRO1013; NREPETIDEYIR.

RRINTS; PRO1013; NREPETIDEYIR.

RRINTS; PRO1013; NREPETIDEYIR.

RRINTS; PROSITE; PRO1013; NREPETIDEYIR.

RRINTS; PRO1013; NREPETIDEYIR.

RRINTS; PRO1013; NREPETIDEYIR.
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1124
68
1136
6
                                           SEQUENCE FROM N.A.
MEDLINE=98096393; PubMed=9434780;
Ringvall M., Berglund M.M., Larhammar D.;
Multiplicity of neuropeptide Y receptors: cloning subtype in the Zebrafish.";
Biochem. Biophys. Res. Commun. 241:749-755 (1997).
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Matches:
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16:1357-1363(1997)
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Best Local Similarity:
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     TCATGSCCATCTGATTCATACAGAATTGCCTTTACTATCTCTTTATTGCTAGTTCAGTAT
                                                                                                    ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGTCTGCAGAAGTATAAAGCTGT
                                                                                                                                   GGATTGTCCAACAAAAAAAAACAGACTTGAAGAAAATGAGATGATCAACTTAACTCTTCAT
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Neuropeptide Y/peptide YY receptor Ya.
Name=npyrya; Synonyms=NPYRYA;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL TaxID=7955;
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BEDLINE=98068842; Pubmed=9407007;
Lundell I., Berglund M.M., Starback P.,
Larhammar D.;
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SEQUENCE FROM N.A.
MEDLINE=22763539; PubMed=12777532;
Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
"Three neuropeptide Y receptor genes in the spiny dogfish, S acanthias, support en bloc duplications in early vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Biol. Evol. 20:1271-1280(2003)
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Best Local Similarity:
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  AATTTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTCTGGACACTAGGTTTTGCC
                                                                                                                                      ThrserLeuProPheLeuAlaPheHisLeuLeuThrSerGluProTyrSerLeuPhePro
                                                                                                                                                                                    GCATTGCTGAGCAGCAGGTATTTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATT
                                                                                                                                                                                                                                191 AlaProLeuSerGlnLeuGlnValCysLeuGluValTrpProSerGlnAspHisLysLeu
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                                                                                          554 ATCTGTTCCCCTTCCAGTGTTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTCA
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Squalus acanthias (Spiny dogfish).
Squalus acanthias (Spiny dogfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Hypnosqualea, Squaliformes, Squaloidei;
NCBI_TaxID=7797;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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	RI acanchias, Support en Bloc Dupli. RI Evolution."; RL Mol. Biol. Evol. 20:1271-1280(20		DR EMBL; AXI/12/3; AAG52565-1; C. DR RESPLOY AXI/72/2; AAG62565-1; JOIN KW Receptor 348 348 FT NON TER 348 348	SEQUENCE 348 AM; 40/38 AW; Grament Scores: 7.73e-35	527.00 Y: 43.30%	1 1 t y ;	1-1406	Qy 29 TCCAAGGAGACTATAATATGGA	Db 19 SerGluArgAsnPheThrLeuAs	36	96 1		Qy 209 GGCTTTATGGGGGATCTACTTAT	Db 52 GlyValSerGlyAsnLeuLeuLe	Qy 269 ACGGTAAACTTCCTCATAGGCAA	Db 72 ValThrAsnileLeuileValA	М	Db 92 LeubroPheThrLeuValTyrTh	112	Qy 449 ATTGCCATTGTCAGGTATCATAT	Db 132 IleAlaValGluArgHisGlnL	Qy 509 CAIGGCTACTTTCTGATAGCTA	Db 152 HisAlaTyrLeuSerileValTr	Qy 569 CCAGTGTTTCACAGTCTTGTGG		Qy 626 AGCAGGTATTATGTGTTGAGT(Db 192 GlyLysTyrMetCysLeuGluG		Db 212 CysLeuLeuValMetGlnTyrP
	569 CCAGIGITICACAGICITGIGGAACITCAAGAAACATITGGITCAGCATIGCTGAGC 625 	626 AGCAGGTATITATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCCTTTACTATC 685	686 TCTTTATTGCTAGTTATTTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGT 745 :::::: 212 CysLeuLeuValMetGlnTyrPheAlaProLeuCysPheIlePheIleCysTyrPheLys 231		SATCAACTTAACTCTTCATCCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGC 86	232 232	6 AGCCATAAATGGAGTTATTCATCATCAAAAAACACAGAAAGATATAGGAAGAAGACA 92	3	2.6 GCAIGIGIGIGIAIACCIGCICCAGARAGACCIIII CAGAGAGACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	986 GAAAACTTTGGCTCTGTAAGAAGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTC 1045	250 250	1046 CCCACTIGCTITGAGAIAAACCTGAAGAAAATTCAGATGTTCATGAATTGAGAGTAAAA 1105	257	CGITCIGITACAAGAATAAAAAGAGATCTCGAAGTGTITTCTACAGACTGACGATACTG 1		1166 ATATTAGTATTTGCTGTTAGTTGGATGCCACTACACCATTTCCATGTGGTAACTGATTT 1225 :::::	Valvatalarhealailetysiipueurioueuasiileemessunavalenoority 20	AsnTyrGluValIleAsnAsnCysHisHisHssnLeuValPheSerIleCysHisLeuThr	GGCAIGAIGICCIGIIGICIIAAICCAAIICIAIAAGGIIICIIAAIAAIGGGAIIAAA 13		6 GCTGATTTAGTGTCCCTTATACAC 13	328 ArgAspLeuArgSerIleLeuHis 335	. Had	AAO82565; PKELIMINANY; FAL; 340 AA:	25-MAR-2004 (TEMBLIEL: 27, Created) 25-MAR-2004 (TEMBLIEL: 27, Last sequence update) 25 MAR-2004 (TEMBLIEL: 27, Last sequence update)	NPY receptor (Imministry 2.) Just ministry of the companies of the compani	Squarts acquientas (opini vogissi). Eukaryote (detazoa, Chordata) (caniata; Vertebrata, Chondrichthyes; Blanchysanchii, Gmislas, Smislaidae, Smislidae, Smislidae	OC BIASHODIANDILI; oquarea, oquareiro oquariano, oquarea. NN NCBI_TaxID=7797; RN [1]	SEQUENCE FROM N.A.
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532;
on E.T., Laxhammar D.;
Genes in the Spiny Dogfish, Squalus
lications in Early Vertebrate
                                                                          lell D.H., Larhammar D.;
M./GenBank/DDBJ databases.
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R InterPro; IPR000276; GPCR Rhodgen.
InterPro; IPR000361; NPY_receptor.
InterPro; IPR000131; NPY_receptor.
R InterPro; IPR00011; NPY_receptor.
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R PRINTS; PR01013; NPEPTIDEVR.
R PRINTS; PR01013; NPEPTIDEVR.
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R PROSITE; PS00237; G_PROTEIN_RECEP_FI_2; I.
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             GTCTGCAGAAGTATAAGCTGTGGATTGTCCAACAAAGAAAACAGACTTGAAGAAATGAG
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AY177271; AAO62564.1; -.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Blasmobranchii; Squalea; Hypnosqualea; Squaliformes; Squaloidei;

Squalidae; Squalus.

NCBI_TAXID=7797;
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                                          1064 AAACCTGAAGAAAATTCAGATGTTCATGAATTGAGAGTAAAACGTTGTGTTACAAGAATA 1123
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - protein search, using frame_plus_n2p model Run on: October 21, 2004, 11:38:29 ; Search time 42 Seconds (without alignments) 4440.148 Million cell updates/sec Title: US-09-771-956-4 Perfect score: 2480	apext 0.5 apext 7.0 lext 7.0 18000 residues	Total number of file satisfying chosen parameters. Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -MODEL=frame+ nZP model - DEV=x1p -MODEL=frame+ nZP model - DEV=x1p -DE_score_1 103738 9400/app query.fasta_1.1543 -DE_ISSUEd_Patents_A -OFWT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 - UNITES=bits -START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi -LISTA5 -DOCALIGN=200 - THR SCORE=pct - THR MAXE=100 - TRR MIN=0 - ALIGN=15 -MODE=LOCAL -OUTPWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USER=USO97171956 GCGN 1 - 146 GRINAT - LISTA5 - DOCALIGN=6 - ICPU=3 -NO MMAP - LARGEQUERY -NEG SCORES=0 -WAIT - DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 - YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7	Issued_Patents_AA:* 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pe 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pe 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pe 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pe 5: /cgn2_6/ptodata/1/iaa/bac/files1 6: /cgn2_6/ptodata/1/iaa/bac/files1 No. is the number of results predicted h	t than or equal to the score of ad by analysis of the total sco SUMMARIES ITY CH Length DB ID	1 2386 96.2 455 PCT-USS5-15646-4 Sequence 4, Appliance 2385 96.2 455 1 US-08-499-025-4 Sequence 4, Appliance 3 2385 96.2 455 2 US-08-566-096A-4 Sequence 4, Appliance 4, Appliance 3 2385 96.2 455 2 US-08-566-096A-4 Sequence 4, Appliance 4, Appliance 4, Appliance 4, Appliance 4, Appliance 4, Appliance 5 2385 96.2 455 4 US-09-200-495-4 Sequence 4, Appliance 5 2385 96.2 455 4 US-09-447-907-4 Sequence 4, Appliance 5 2330 94.0 445 2 US-08-630-118A-6 Sequence 6, Appliance 5 2330 94.0 445 2 US-08-03-199-21 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6, Appliance 6 2330 94.0 445 3 US-09-235-839-6 Sequence 6 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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ALIGNMENTS

REBULT.

PCT-US95-15646-4

| PCT-US95-15646-4
| Sequence 4, Application PC/TUS9515646
| TITLE OF INVENTION: WERTHORS OF WODIFTING FEEDING BEHAVIOR, COMPOUNDS TITLE OF INVENTION: V/PERTIDE YY RECEPTOR (YS) AND USES THEREOF TITLE OF INVENTION: V/PERTIDE YY RECEPTOR (YS) AND USES THEREOF TITLE OF INVENTION: V/PERTIDE YY RECEPTOR (YS) AND USES THEREOF TITLE OF INVENTION: V/PERTIDE YY RECEPTOR (YS) AND USES THEREOF TITLE OF INVENTION: V/PERTIDE YY RECEPTOR (YS) AND USES THEREOF TITLE OF INVENTION: V/OF AND TITLE OF INVENTION: V/OF AND TITLE OF INVENTION OF AND TITLE OF A

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TOPOLOGY: linear MOLECULE TYPE: protein CT-US95-15646-4	Alignment Scores: 3.78e-270 Length: 456 Score: 2386.00 Matches: 456 Percent Similarity: 100.00% Conservative: 0 Query Match: 56.21% Indels: 0 DB: 5	109-771-956-4 (1-1406) x PCT-US95-15646-4 (1-456)	AGGACTICACATAGA ATATACTCACGCCACTCGGATTCTGATTCTCCAGTCTGG INTILITIALITIALITIALITIALITIALITIALITIAL	ATTT	197 GTAAGTCTTCTTGGCTTTATGGGAATCTACTTATTTAATGGCTCTCATGAAAAAGCGT 256 	257 AATCAGAAGACTACGGTAAACTTCCTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTT 316 	317 GTGCTGTTTTGCTCACCTTTCACACTGTCTGTCTTGCTGGATCAGTGGATGTTTGGC 376	377 AAAGTCATGGCCATATTATGCCTTTTCTTCAATGTGTGGCAGTTTTGGTTTCAACTTTA 436 	. 437 ATTTTAATAICAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT 496	497 TTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTCTGGACACTAGGTTTTGCCATC 556	557 IGTICICCCCTICCAGIGTITCACAGICTIGIGGAACTICAAGAAACATITGGITCAGCA 616 	617 TIGCTGAGCAGCAGTATTATGTGTTGAGCCATCTGATTCATACAGAATTGCC 676 	677 TTTACTALCTCTTTATTGCTAGTTCAGTATATTCTGCCCTTAGTTTGCCTTACTGTAAGT 736 	737 CATACAAGTGTCTGCAGAAGTATAAGCTGTGGATTGTCCAACAAAGAAAACAGACTTGAA 796 	797 GAAAAIGAGAIGATCAACTIAACTCTTCATCCAAAAAGAGTGGGCCTCAGGTGAAA 856 	857 CTCTCTGGCAGCCATAAATGGAGTTATTCATTCAAAAAACACAGAAGAAGAAGATATAGC 916

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17.112 OF INVENTION: Richard L. PERRIDOS OF WOLFYING FEEDING BEHAVIOR, AMD DNA ENCODING A HYPOTHALAN TITLE OF INVENTION: NETHODS OF WOLFYING FEEDING BEHAVIOR, NETHODS OF WOLFYING SEEPING BEHAVIOR, NETHODS OF WOLFYING SUPERIOR OF INVENTION: NETHODS OF WOLFYING STREET: LISS AND USES THEREOF CORRESPONDING A DUNDAM LLP STREET: LISS AND USES THE OF INVENTION: NETHODS OF WOLFYING STREET: LISS AND USES THE OFFICE OF INVENTION: OF INVENT
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Matches:
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                                                           4.94e-270
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100.00%
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-349-025-4
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Best Local Similarity:
Query Match:
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Sequence 4, Application US/08668650B

Detert No. 598920

GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Waker, Mary W.
APPLICANT: Waker, Mary W.
APPLICANT: Wainshank, Richard L.
TITLE OF INVENTION: Methods of Modifying Feeding Behavior,
TITLE OF INVENTION: Compounds of Modifying Feeding Behavior,
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                       LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg
                                                                              ATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCAGTAAGTTCATA
                                                                                                321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerSerLysPheIle
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                       AAGAAGACAGCATGTGTTACCTGCTCCAGAAAGACCTTCTCAAAGAACCACTCCAGA
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INGUINT 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION NUMBER: US/08/668,650B
FILING DATE: 04-JUN-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: White ESG., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166C
TELECHOME: 212-278-0400
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FR: 1795/46166C
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1185 Avenue of the Americas
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SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acid
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STREET: 11
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US-09-200-673-4

i Sequence 4 Application US/09200673A

patent No. 6316203

GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Weinshank, Richard L.
APPLICANT: Weinshank, Theresa
TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useft;
TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (YS)
TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (YS)
TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (YS)
TITLE OF INVENTION ON WHERE: US/09/200,673A
CURRENT FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-20

EARLIER FILING DATE: 1994-12-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1
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                    341 ProGlyValProThrCysPheGlulleLysProGluGluAsnSerAspValHisGluLeu
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Pred. No.:
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      ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-668-650B-4
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Oy 1157 ACCATACTGATATTAGTATTTGCTGTTAGTT	NESULT 6 US-09-194-895-4 US-09-194-895-4 Sequence 4, Application US/09194895 Patent No 6531287 GENERAL INFORMATION: APPLICANT: Gerald, Christophe P.G. APPLICANT: Wainshank, Richard L. APPLICANT: Wainshank, Richard L. APPLICANT: Wainshank, Theresa TITLE OF INVENTION: Methods of Modifying F. TITLE OF INVENTION: MATOR OF CT-US/UPW/BJ. CURRENT FILING DATE: 1999-09-27 PRIOR PRIOR APPLICATION NUMBER: PCT/US97/09504 NUMBER OF SEQ ID NOS: 24 SEQ ID NO 4 LENGTH: 455 TYPE: PRT CORGANISM: Homo sapiens US-09-194-895-4	Alignment Scores: Pred. No.: 2385.00 Matche Score: Percent Similarity: 100.00\$ Conser Best Local Similarity: 100.00\$ Mismat Query Match: 4.17\$ Gaps:	US-09-771-956-4 (1-1406) x US-09-194-895-4 (1 US-09-771-956-4 (1-1406) x US-09-194-895-4 (1 US-09-194-895-4 (1 US-08-194-895-4 US-08-194-895-4 (1 US-08-194-895-4 US-08-194-895-4 US-08-194-895-4 US-08-194-8 US-08-1
1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20 77 AAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCAGTCTGG 136 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40 137 GATCACTATAAAAGCAGTCTAGATCACTACAGTATTTCTGATTGGGCTCTATACATTT 196 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60 197 GTAAGTCTTCTTGGCTTTATGGGGAATCTACTTATTTTAATGGCTCTCATGAAAAGCGT 256 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetLysLysArg 80 257 AATCAGAAGACTACGGTAAACTTCCTCATAGGCAATTTCGATTTTCAATATCTTTTTTGATTTTTTTT	GIGGTGTTTTGCTCACCTTTCACACTGACGTCTTGCTGGATCACTGGATGTTTGGC	7 TTTACTATCTCTTTATTGCTAGTATATTCTGCCCTTAGTTTGTCTTACTGTAGT 73	797 GAAAATGGGTTGACTTGATCATCATCAAAAAGAGTGGGCCTGGAAA 856 261 GludsnoluwetiledanLeuthrLeuhisProcetrysSerGlyProGlnVallys 280 261 GludsnoluwetiledanLeuthrLeuhisProcetrysSerGlyProGlnVallys 280 857 CTCTCTGGCAGCCATAAATGGAGTTATTCATTCATAAAAACACAGAAGAAATATGG 916 281 LeuSerGlySerHisLySTrpSerTyrSerPheileLySLySHiSArgArgArgArgArgG 916 281 LeuSerGlySerHisLySTrpSerTyrSerPheileLySLySHiSArgArgArgArgArgArgArgArgArgArgArgArgArgA
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STTGGATGCCACTACACCTTTTCCATGTGGTA 1216 TAGGCATTTCAAGTTGGTGTATTGCATTTGT 1276 TAATCCAATTCTATATGGGTTTCTTAATAAT 1336 g Feeding Behavior, Compounds Useful 1d DNA Encoding A Hypothalamic 1de Y/Peptide YY Receptor (Y5) 18JA TGCCACTCGGAATTCTGATTTCCCAGTCTGG 136 ACAGTATTTTCTGATTGGGCTCTATACATT 196 ACTTATTTTAATGGCTCTCATGAAAAGCGT 256 AGGCAATCTGGCCTTTTCTGATATCTTGGTT 316 STCTGTCTTGCTGGATCAGTGGATGTTTGGC 376 TATGGATTTAGAGCTCGACGAGTATTATAAC 76 ACACTGTCTTCATATG 1381 4 4 0 0 0 0 R R R R Jth: ches: servative: natches: (1-455)

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Sequence 7, Application US/10013846

Patent No. 656636

Patent No. 6566367

APPLICANT: Bakthavatchalam, Rajagopal

APPLICANT: Barielmann, Harry L

APPLICANT: Brielmann, Harry L

APPLICANT: Brielmann, Harry L

APPLICANT: Brielmann, Alan

APPLICANT: Tran, James W

APPLICANT: Tran, Jennifer

APPLICANT: Sliott, Richard L

APPLICANT: Spirolisobenzofuran-1,4'-piperiding-

APPLICANT: Spirolisobenzofuran-1,4'-piperidines

FILE REFERENCE: NOO.2001

CURRENT APPLICATION NUMBER: US 60/254,990

PRIOR PILING DATE: 2001-12-11

PRIOR FILING DATE: 2001-12-12

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SER ID NOS: 17
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                                                     AAAGICAIGIGCCAIATIAIGCCITITICIICAAIGIGIGIGICAGITIIGGITICAACITIA
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; NUMBER OF SEQ ID NOS: 24 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 4 ; LENGTH: PRT ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Human Y5 CDNA clone US-09-447-907-4	Alignment Scores: 4.94e-270 Length: 455 Score: 2385.00 Matches: 455 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 4 Gaps: 0	US-09-771-956-4 (1-1406) x US-09-447-907-4 (1-455) QY	eProva CTATAC CTATAC UTYFTH GAAAAA	Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuleLeuMetAlaLeuMetLysLysArg 80 Oy 257 AATCAGAAGACTACGTAAACTTCCTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTT 316 Db 81 ASnGlnLySThrThrValAsnPheLeulleGlyAsnLeuAlaPheSerAsplleLeuVal 100 Oy 317 GTGTTTTGGCTCACCTTTTCACACTGCTTTTGTGAATCAGTGGATGGGTTGGTGATTGGC 376	101 ValleuPheCysSerPredefiniteIIIIIIIIIIIIIIIIIIIIIIIII	4 4 4 6 4 9 4 9 4 9 9 4 9 9 9 9 9 9 9 9	Oy 557 TGTTCTCCCTTCCAGTGTTTCACAGTCTTGTGGAACTTCAGGAACATTTGGTTCAGGA 616	OY 677 TITACTATCTCTTATTGCTAGTTCAGTATATTCTGCCCTTAGTTTGTCTTACTGTAAGT 736	797
557 IGITCTCCCCTTCCAGTGTTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTCAGCA [Oy 677 TTTACTATTCTTAATTGCTAGTTCAGTATATTCTGCCCTTAGTTTGTCTTACTGTAGT 736	261 GludanGuMetIledanLeuThrLeuHisProSerIysLysSerGlyProGlnValLys 857 CTCTCTGGCAGCATAAATGGAGTTATTCATCAAAAAAAAA	301 LysLysThralaCysValLeuProalaProGluArgProSerGlnGluAsnHisSerArg 32 977 ATACTTCCAGAAAACTTGGCTCTGTAAGAAGTCAGCTCTCTCT	341 ProdlyvalProthrCysPheGluIleLysProgluGluAmSerAspvalHisGluLeu 360 1097 AGAGTAAAACGTTCTGTTACAAGAATAAAAAGAGATCTCGAAGTGTTTTCTACAGACTG 115 161 AGGVALYSAxGSerValThrAxglleLysAxgSerArgSerValPheTyrAxgluEu 380	Cy 1157 ACCATACTEATATTAGTATTTGCTGTTAGTTGGAGTGCCACTACACCTTTCATGTGAGTA 1216 Db 381 ThrileLeulleLeuValpheAlavallTpmetProLeuHisLeuPheHisValval 400 Cy 1217 ACTGATTTAATGACAATTTCAATAGGCATTTCAAGTTGGTGATTTGCTTTGT 1276 Db 401 ThrAspPheAsnAspAsnLeulleSerAsnArgHisPheLysLeuValTyrCysIleCys 420	Qy 1277 CATTTGTTGGCCATCATGTTCTTAATCCAATTCTATATGGCTTTCTTAATAAT 1336 Db 421 HisbeuleuGlyMetMetSerCysCysLeuAsnProlleLeuTyrGlyPhebeuAsn 440 Qy 1337 GGGATTAAAGCTGATTTAGTGCTCTTAATACACTTCATATG 1381 Db 441 GlyTleLysAlaAsbLeuValSerLeuLeHsisCysLeuHsMet 455	RESULT 8 US-09-447-907-4 ; Sequence 4, Application US/09447907 ; Patent No. 64473774 ; GENERAL INFORMATION ; APPLICANT: Gerald, Christophe P.G.	APPLICANT: Walker, Mary W APPLICANT: Walker, Mary W APPLICANT: Branchek, Theresa ITILE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful in Such M ITILE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful in Such M ITILE OF INVENTION: and DNA Encoding A Hypothalamic Atypical Neuropeptide Y/Peptide FILE REFERENCE: 1795-46166CA CURRENT APPLICATION WHBER: US/09/447,907	; PRIOR APPLICATION NUMBER: 08/668,650 ; PRIOR FILING DATE: 1996-06-04

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Matches:
Conservative:
Mismatches:
Indels:
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TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acids
TYPE: mino acid
MOLECTLE TYPE: protein
US-08-630-118A-6
                                                                                                                                      1.34e-263
2330.00
100.00%
100.00%
93.95%
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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US-08-6530-118A

Sequence 6, Application US/06630118A

Patent No. 5319901

GENERAL INFORMATION: Vinghe
APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Daime R.
APPLICANT: Bloomquist Ph.D., Linda J.
APPLICANT: Bloomquist Ph.D., Linda J.
APPLICANT: Cornfield Ph.D., Linda J.
CONTESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
SIREET: 300 South Wacker Drive, 32nd Floor
CONTES: McDonnell Boehnen Hulbert & Berghoff
SIREET: 300 South Wacker Drive, 32nd Floor
CONTES: Libert Compatible
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAPPLICATION DATA:
APPLICATION NUMBER: US/08/630,118A
FILING DATE: April 8, 1996
CLASSIFTATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGATTAAAGCTGATTTAGTGCCCTTATACACTGTCTTCATATG 1381
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US-08-630-118A-6
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                           1.34e-263
2330.00
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              TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 (312)715-1000
                                                         LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                     MOLECULE TYPE: protein US-08-838-399-6
                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
 TELEPHONE:
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                                            TTCATCAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTTACCTGCTCCA
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GENERAL INFORMATION:

APPLICANT: Hu Ph.D., Vinghe

APPLICANT: Hu Ph.D., Michael L.

APPLICANT: Bloomquist Ph.D., Brian T.

APPLICANT: Flores-Riveros Ph.D., Jaime R.

APPLICANT: Cornfeld Ph.D., Linda J.

TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

TITLE OF INVENTION: Sequences

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRI:

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATENTING RELEASE #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: US/08/838,399
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-838-399-6
; Sequence 6, Application US/08838399
; Patent No. 5965392
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SEQUENCE CHARACTERISTICS: LENGTH: 445 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-09-003-199-21	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: 100.00\$ Mismatches: Query Match: 2,95\$ Gaps:	US-09-771-956-4 (1-1406) x US-09-003-199-21 (1-445)	107 GCCACTCGGAATTCTCAGTCTGCATCTGCATGATAAAAGCAGTGTAGATAA 16	Db 21 AlaThracgashSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40 Qy 167 CAGTATTTTGATTGGCTCTATACATTTGTAGAGTTTAGAGTTTAGAGTTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGAGTTAGAGAGAGTTAGAGAGAGTTAGAGAGAGTTAGAGAGAGTTAGAGAGAGTTAG	Db 41 dlnfyrheleulledlyLeufyrfhrhlyndlychemetGlydsnleu 60 227 CTTATTTTAAGGCTCTGTGAAAAGGGTAATCAGAAGACTACGGTAAACTTCTCTATA 286	Db 61 LeulleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeulle 80 Qy 287 GGCAATCTGGCTTTTCGATATCTTGGTTTTGCTCACCTTTCACACTGGCG 346	Db 81 GlyAshLeuAlaPheSerAspileLeuValValLeuPheCysSerProPheThrLeuThr 100 Qy 347 TCTGTCTTGCTGGATCGATGTTTGGCAAAGTCATGTGGCATATTAGCCTTTTTCTT 406	Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120	Qy 407 CAAIGIGIGCAGIIIIGGIIICAACIIITAAITITAAIAIGCCAIIGICAGGIAI 466	Qy 467 CATATGATAAAACATCCCATATCTAATAATTTAACAGCAAACCATGGCTACTTTCTGATA 526	Oy 527 GCTACTGTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTCACAGTCTT 586	Oy 587 GTGGAACTTCAAGAACATTTGGTTGACCAGCAGCAGGTATTTATGTGTTGAG 646	Oy 647 TCATGGCCATCTGATTCATACAGAATTGCCTTTACTACTTATTGCTAGTTCAGTAT 706	Qy 707 ATTCTGCCCTTAGTTTGTCTTACTGTAGTCATACAAGTGTCTGCAGAAGTATAAGCTGT 766	Qy 767 GGATTGTCCAACAAAGAAAACAGACTTGAAGAAAATGAGATGATCAACCTTAACTCTTCAT 826	Oy 827 CCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTATTCA 886	
	Qy 947 GAAAGACCTTCTCAAGAAACCACTCCAGAAAACTTCGGTGTAAGA 1006 Db 301 GluArgProSerGlnGluAsnH1sSerArglleLeuProGluAsnPheGlySerValArg 320 Qy 1007 AGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATAAA 1066 Db 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340	ď	rodiudinasiiseraspvalrisejuheuargyallyskrigservalinralgilelys 3 Agagalctcgaagrottttcpacagactgaccatactgatattagtatttgctctpagt 1 	Qy 1187 TGGATGCCACTACATTTCCATGTGGTAACTGATTTTAATGACAATCTTATTTCAAAT 1246	Oy 1247 AGGCATTTCAAGTGGTGTATTGCATTTGTCATTTGTTGGGCATGATGTCCTGTTGTTT 1306	OY 1307 AATCCAATTCTATAATGGGTTTCTTAATAGGGATTAAAGCTGATTTAGTGTCCCTTATA 1366	Qy 1367 CACTGTCTTCATATG 1381 	RESULT 11	21, 21, 5, 59 INFC	, APPLICANT: Parker, Eric M ; APPLICANT: Strader, Catherine D ; APPLICANT: Rudinski, Mark S ; TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY YS RECEPTORS	OF PONI ESSI ET:		; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette ; COMPUTER: Apple Macintosh ; OPERATING SYSTEM: Macintosh ;		~	REFERENCE/DOCKET NUMB: TELECOMMUNICATION INFOR: TELEPHONE: (908)298-53	IN

TELEPHONE: (312)913-0001 TELEFAX: (312)913-0002 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: ISNGTH: 445 amino acid TYPE: anino acid TYPE: anino acid TYPE: anino acid MCTOBOLOGY: linear MCTOBOLOGY: linear MOLECULE TYPE: protein US-09-235-839-6 Length: 445 Pred. No: 2330.00 Macches: 445 Precent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3 US-09-771-956-4 (1-1406) x US-09-235-839-6 (1-445)	Oy 17 AIGGATTTAGAGCTCGACGAGTATTATAACAAGACACTTGCCACAGAGAATAATACTGCT 106 Db 10 MetaspleuGluleuAspGluTyTyTyAsnLySThrLeuAlaThrGluAsnAsnThrAla 20 Oy 107 GCCACTCGGAATTCTGATTTCCCAGTCTGGGATGACTAAAAGCAGTGTAGATGACTTA 166 Db 21 AlaThrArgAsnSerAspPheProvalTrpAspAspCytLysSerSerValAspAspLeu 40 Oy 167 CAGTATTTCTGATTGGGCTCTATACATTGTAAAGCAGTGGAATGTA 226 I67 CAGTATTTCTGATTGGGCTCTATACATTGTAAGTCTTTTTGGGGGAATGTA 226 16 CAGTATTTTCTGATTGGGCTCTATACATTGTAAGTCTTTTTTTT	Qy 287 CTTATTTTAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAACTTCCTCATA 286	407 CATALOGUES OF THE CONTROLL	Qy 647 TCATGGCCATCTGATTCATACAGAATTGCCTTTACTATTGCTAGTTCAGTAT 706 Db 201 SerTrpProSerAspSerTytArg1leAlaPheThrIleSerLeuLeuLeuLeuValGlnTyr 220 Qy 707 ATTCTGCCCTTAGTTTGTCTTACTGAAGTCATACAAGTGTCTGCAGAAGTATAAGCTGT 766 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCySargSerIleSerCys 240 767 GGATTGTCCAACAAAAAAAGAGCTTGAAGAAAATGAGATGATCAACTTAACTTTACTTTGATGAGTATAAGTGTTTAGTTAGTTAGTTAGTTAGTTAGTTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTAG
OY 887 TTCATCAAAAAACACCAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTTACCTGCTCCA 946 Db 281 PhellelysLy8HisArgArgTyzSerLy8Ly8ThrAlaCysValLeuProAlabro 300 QY 947 GAAAGACTTCTCAAGAGAACCACTCCAGAATACTTCCAGAAACTTTGGCTCTGTAAGA 1006 301 GluArgProSerGlnGluAshHisSerArgIleLeuProGluAshPheGlySerValArg 320 QY 1007 AGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGTAAAA 1066 Db 321 SerGlnLeuSerSerSerSerSerJerFl	Oy 1187 TGGATGCCACTACACCTTTCCATGTGGTAACTGATTTTAATGACAATCTTATTCAAAT 1246 Db 381 TrpMetProLeuHisLouPheHisValValThrAspPheAsshAspAshLeuIleSerAsn 400 Qy 1247 AGGCATTCAAGTTGGTGTATTGCATTTGTTGGGCATGATGTCTTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	Qy 1367 CACTGTCTTCATATG 1381 Db 441 HisCysLeuHisMet 445 RESULT 12 10.09-235-839-6 Secont No. 620799 6207799 GENERAL INFORMATION: APPLICANT: McCaleb Ph.D., Michael L. APPLICANT: McCaleb Ph.D., Michael L. APPLICANT: Bloomquist Ph.D., Michael L. APPLICANT: Ployee Diverse Ph.D., Jaim P. Applicant Ph.D., Jaim P.	APPLICANT: Flores-thveros Ph.D., Jalme K. APPLICANT: Cornfield Ph.D., Linda J. ITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid ITLE OF INVENTION: Sequences TITLE OF INVENTION: Sequences NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSES: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive, 32nd Floor CITY: Chicago STREET: 1L COUNTY: USA ZIP: 60606 COMPUTER READALLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible	OPERATING SYSTEM: SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/235,839 FILING DATE: BAPLICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/630,118 PILING DATE: APPLICATION: NAME: Greenfield Ph.D., Michael S. RESISTATION NUMBER: 37,142 RESISTATION NUMBER: 96,149-C TELECOMMUNICATION INFORMATION:

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GGATTGTCCAACAAAAAAAAAGACTTGAAGAAAATGAGATGATCAACTTAACTCTTCAT 826
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 37,147
REPERBRUCE/DOCKET NUMBER: 96,149/WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
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ON
                                                                                                         | LENGTH: 445 amino acids | TYPE: amino acids | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID US-09-327-035-6
                                                            TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
Query Match:
DB:
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CORRESPONDENCE ADDRESS:
STREET: 10.00 South Wacker Drive
CITY: Chicago
CITY: Chicago
CITY: Chicago
CITY: Chicago
CONTRY: 11.
COUNTRY: USA
ZIP: 6606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFRRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/327,035
FILING DATE: 07-Jun-1999
CLASSIFICATION NUMBER: US/09/327,035
FILING DATE: 07-Jun-1999
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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Patent No. 6368824
GENERAL INFORMATION:
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241 GlyLeuGerAshiysGluAshargLeuGluGluAsnGluMerlieAnnLeuthrieuHis 260 Qy 827 CCATCCAAAAGAGTGGGCCTCAGGTGAAACTCTGGCAGCATAAATGGAGTATTCA 886 Db 261 ProSerlySiysGerGlyProGluValLySieuGserGlySerHisLySTrpGerTyrSer 280 Qy 887 TTCATCAAAAACACAAGAAGATATAACAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	RESULT 14 US-09-065-027-2 Sequence 2, Application US/09065027 Patent No. 6528303 GENERAL INFORMATION: TITLE OF INVENTION: NEUROPEPTIDE Y-Y5 RECEPTOR FILE REPERENCE: 27340201800 CURRENT FILING DATE: 1998-04-22 FRIOR PEPLICATION NUMBER: US/09/065,027 CURRENT PILING DATE: 1998-04-22 PRIOR PELING DATE: 1998-11-08 NUMBER: OF SEQ ID NOS: 8 NUMBER: PatentIN Ver. 2.1 LENGTH: 445 COGANISM: Homo sapiens Alignment Scores: Precent Similarity: 100.00% Matches: 0 Best Local Similarity: 100.00% Mismatches: 0 Gouery Match: 445 COG-771-956-4 (1-1406) x US-09-065-027-2 (1-445)

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Conservative:
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US-09-708-392-13
Sequence 13, Application US/09708392
Sequence 13, Application US/09708392
Sequence 13, Application US/09708392
Sequence 13, Application US/09708392
APPLICANT: Pizer Inc
APPLICANT: Pizer Inc
APPLICANT: Maw, G
TITLE REPERBNCE: PC10343AAM
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT APPLICATION NUMBER: GB 9926437.6
PRIOR PELICYTION NUMBER: GB 0004021.2
PRIOR PELICYTION NUMBER: GB 0004021.2
PRIOR PELICYTION NUMBER: GB 0013001.3
PRIOR PELICYTION NUMBER: GB 0013001.3
PRIOR PELICY SOUPO-02-18
PRIOR APPLICATION NUMBER: GB 001141.3
PRIOR PELICY SOUPO-02-16
PRIOR PELICY SOUPO-02-16
PRIOR PELICY DATE: 2000-07-05
PRIOR PELICY PORTION NUMBER: US 60/175,161
PRIOR PELICY PORTION NUMBER: US 60/175,161
PRIOR PELICY PORTION NUMBER: US 60/221,014
PRIOR PELICY DATE: 2000-07-11
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ORGANISM: Homo sapiens
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Query Match:
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Search completed: October 21, 2004, 12:01:22 Job time : 65 secs

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Sequence:

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Sequence 6, Appli
Sequence 205, Appli
Sequence 668, Appli
Sequence 668, Appli
Sequence 614, Appli
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Sequence 20, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 25, Appl
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Sequence 23, Appl
Sequence 23, Appl
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Sequence 378, App
Sequence 330, Appl
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Sequence 31, Appl
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Sequence 746, App
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Patent No. US20010031474A1
GENERAL INFORMATION:
APPLICANT: Bennett, Michele
APPLICANT: Brobbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors;
FILE REFERENCE: N2000.001;
CURRENT APPLICATION NUMBER: US/09/771,956;
CURRENT APPLICATION NUMBER: 2001-01-29;
NUMBER OF SEQ ID NOS: 31;
SOFTWARE: PatentIn Ver. 2.1
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US-10-10-10-47-37-8
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US-10-309-115-10
US-10-10-70-393-33
US-10-10-70-391-10
US-10-291-990-31
US-10-295-027-640
US-10-295-027-746
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US-10-10-648-4
US-10-081-810-50
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Matches:
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2385.00
 ORGANISM: Homo sapiens
Alignment Scores:
Pred. No.:
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LENGTH: 455
TYPE: PRT
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US-09-771-956-13
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-MODEL=frame+ n2P.model -DEV=xlp
-CgnZ 1/USFTO spool p/US09771956/runat_21102004 103739 9430/app query.fasta_1.1543
-DS=Published Applications AA -OFMT=fastan -SUFFIX=n2P.rapb -MINNATCH=0.1
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-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=PCD -NORM=ext -HBARSIZE=500 -MINIEN=0
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1. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCONB.pep:*

2. /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3. /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

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19. /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                            October 21, 2004, 11:40:49 ; Search time 186 Seconds
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                         protein search, using frame_plus_n2p model
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Db 321	1157 ACCATACTGATATTTGCTGTTAGTTGGATGCCACGTACACCTTTTCCATGTGGTA 121	Oy 1217 ACTGATTTTAATGACAATTCTTAATGACAATTCCAATTGCAATTCCTATTCCAATTCCTATTCCAATTCCTATTCCAATTCCTATTCCAATTCCTATTCCAATTCCTATTCCAATTCCTATTCCTATTCCTATTCCTATTCCTATTCCTATTCCTATTCCTATTCCTATTCCTATTCCTATTCTATTCTTATTTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCTTATTCT	421 HisLeuleuGlyMetMetSerCysCysLeuAsnProlleLeuTyrGlyPheLeuAsnAsn 440	441 GlylleLysAlaAspLeuValSerLeulleHisCysLeuHisMet 45	RESULT 6. US-09-962-646-4 ; Sequence 4, Application US/09962646 ; Patent No. US/0020103123A1 ; CENTER 1 TAPPERATION	; APPLICANT: GERALD, CHRISTOPHE P.G. ; APPLICANT: WEINSHANK, RICHARD L ; APPLICANT: WALKER, WARY W ; APPLICANT: WALKER, WARY W	JEPLICANT: BRANCHEAK, HEREBA JITLE OF INVENTION: WODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND JITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPT JEILE REFERENCE: 1795/46166EZA	CURRENT FILING DATE: 2001-09-24 ; PRIOR APPLICATION NUMBER: 09/200,673 ; PRIOR TILING DATE: 1998-11-25 ; PRIOR TILING DATE: 1998-11-20	FRICK PELLICATION NOMBER: 08/300,030 FRICK FILING DATE: 1995-12-01 FRICK APPLICATION NUMBER: 08/349,025 FRICK FILING DATE: 194-12-01	NOWING OF SECULIA VERSION 3.1 SEQ ID NO 4 : LENGTH: 455) AIRS AND Sapiens US-09-962-646-4	Alignment Scores: Pred No.: Score: 3.11e-223 Length: 455 Score: 2385.00 Matches: 455 Preent Similarity: 100.00% Conservative: 0 Percent Similarity: 100.00% Nirmather: 0	96.17\$ Institutions: 9 Gaps: 9 Gaps:	ACTATAATA	77 PAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGATTTCCCAGTCTGG	Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPhebrovalirp 40 Qy 137 GATGACTATAAAAGCAGTGTAGATTACAGTATTTCTGATTGGGCTCTATACATTT 196
Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 96.17% Indels: 0 DB: 9 Gaps: 0 US-09-771-956-4 (1-1406) x US-09-771-956-13 (1-455) 0 QY 17 ATGTCTTTTATTCCAAGGAGGACTATAATAGGATTTAGAGCTCGAGGAGTATTATAAC 76	Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20 Qy 77 AAGACACTTGCCACAGAGAATAATACTGCTGCCACTCGGAATTCTGCATTTCCCAGTCTGG 136 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40	Oy 137 GATGACTATAAAAGCAGTGTAGATGATTACAGTATTTTCTGATTGGGCTCTATACATTT 196	Qy 197 GTAAGTCTTCTTGGCTTTATGGGGAATCTACTTATTATAATGGCTCTCATGAAAAGCGT 256 [Qy 257 AATCAGAACACTACGTAAACTTCCTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTT 316	Oy 317 GIGGIGITINGCICACCITICACAGIGACGICTGICTIGCIGGATCAGIGGAIGITIGGG 376	Qy 377 AAAGTCATGTGCCATATTATGCCTTTTCTTCAATGTGTGTCAGTTTTGGTTTCAACTTTA 436	Qy 437 AITTAATAICAATIĞCCALIGICAGGIAICAIAIGAIAAAACKICCCATAICTAATAAI 496 Db 141	Oy 497 TTAACAGCAAACCATGGCTACTTTCTGATAGCTACTGTCTGGACACTAGGTTTTGCCATC 556	OY 557 TGTTCTCCCCTTCCAGTGTTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTCAGCA 616	Qy 617 TTGCTGAGCAGCAGCATATTTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCC 676 Db 201 LeuleuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArg1leAla 220	Oy 677 TITACTATCTITATIGCTAGTICAGTATATICTGCCCTTAGTITGTCTTACTGTAAGT 736	Qy 737 CATACAAGTGTCTGCAGAAGTATAAGCTGTGGATTGTCCAACAAAAAAAA	Oy 797 GAAAATGAGATGATCAACTTAACTCTTCATCCAAAAAGAGTGGGCCTCAGGTGAAA 856	Qy 857 CTCTCTGGCAGCCATAAATGGAGTTATTCATTCATCAAAAAACACAGAAGAAGAATATAGC 916	Qy 917 AAGAAGACATGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA 976 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 977 ATACTTCCAGAAACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTCATA 1036

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41 AspablyLySerSerValAspaseLenGintyPriseLeulicityLeuryPrizePe 60 52 TOTAL TOT	341 ProdlyValProThrCysPheGluIleLysProGluGludsnSerAspValHisGluLeu 360 1097 AGAGTAAAACGTTCTGTTACAAGAATAAAAAGAGATCTCGAAGTGTTTTCTACAGACTG 115 1097 AGAGTAAAACGTTCTGTTACAAGAATAAAAAGAGATCTCGAAGTGTTTTCTACAGACTG 115 1157 ACCATACTGAATTTAGTATTTGTTGTTGGATGCCACACACCTTTTCCATGTGGT 121 1157 ACCATACTGAATTTAGTATTTCAAATAGGATGCCACACACCTTTTCCATGTGGT 121 1151 ACCGATTTTAATGACATTTCAAATAGGCATTTCAAGTGGTGTT 120 1217 ACTGATTTTAATGACAATCTTATTTCAAATAGGCATTTCCAAGTGGTTTTCCATTTGT 127

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TIGCCACTCGGAATTCTGATTTCCCAGTCTGG 136
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GENERAL INFORMATION:

APPLICANT: Bakthavatchalam, Rajagopal
APPLICANT: Blum, Charles A.

APPLICANT: Blum, Charles A.

APPLICANT: Blum, Tharry L.

APPLICANT: Briefmann, Harry L.

APPLICANT: Briefmann, Harry L.

APPLICANT: Thutchines W.

APPLICANT: Than, Jennifer W.

APPLICANT: Than, Jennifer W.

APPLICANT: Than, Jennifer W.

APPLICANT: Bliott, Richard L.

APPLICANT: Done Lower L.

APPLICANT: Bliott, Richard L.

APPLICANT: Richard L.

APPLICANT: Bliott, Richard L.

APPLICANT L.

APPLICANT: Bliott, Richard L.

APPLICANT: Bliott, Richard L.

APPLICANT: Bli
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TYPE: PRT
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Sequence 7, Application US/10410648
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Patent No. USCOLO031474Al

GENERAL INFORMATION:

APPLICANT: Bennett, Michele

APPLICANT: Brodbeck, Robbin

APPLICANT: Krause, James

TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors

FILE REFERENCE: NO2000.001

CURRENT FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 455
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                CAGIAITITCIGAITGGCCTCTAIACAITIGIAAGICITCITGCTTTAIGGGGAAICTA
                            CTTATTTTAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAACTTCCTCATA
                                                                                          LeulleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeulle
                                                                                                                                                                                                                                                           407 CAATGIGIGICAGITITIGGITICAACTITIAAITITAAIAICAATIGCCAITGICAGGIAĮ
                                                                                                                                                                                                                                                                                                                                                                                                                                          587 GTGGAACTICAAGAAACATTIGGTICAGCATIGCTGAGCAGCAGGTATTTATGTTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer
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                                                                                                                                   GGCAATCTGGCCTTTTCTGATATCTTGGTTGTGTTTTTGCTCACGTTTCACACTGACG
                                                                                                                                                                                               TCTGTCTTGCTGGATCAGTGGATGTTTGGCAAAGTCATGTGCCATATTATGCCTTTTTCTT
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ThraspPheasnaspasnLeulleSerasnargHisPheLysLeuvalTyrCyslleCys
                                                              421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProlleLeuTyrGlyPheLeuAsnAsn
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MCCaleb Ph.D., Michael L.

Bloomquist Ph.D., Brian T.
Flores-Riveros Ph.D., Jaime R.

Cornfield Ph.D., Linda J.

TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
Sequences
                                                                                                     GGGATTAAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: LIL
COUNTRY: USA
ZIP: 60606
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,049
FILING DATE: US/806
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-771-956-4 (1-1406) x US-10-027-049-6 (1-445)
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                                              CATTIGITGGGCATGATGTCCTGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID US-10-027-049-6
                                                                                                                                                                                               ; Sequence 6, Application US/10027049; Publication No. US20030022283A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 445 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (312)715-1234
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
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Percent Similarity;
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Query Match:
DB:
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Pred. No.:
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US-10-027-049-6
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1947 - 1967 - 1967 - 1967 - 1968 - 19	Š	CTAATAATTTAACAGCAAACC
ArgHisPhelysLeuvalTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu	G Q	HismetileLysHisProlleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeulle
1307 AATCCAATTCTATATGGGTTTCTTAATAATGGGATTAAAGCTGATTTAGTGTCCCTTATA 1366 	65 G	527 GCTACTGTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTCACAGTCTT 586
1367 CACTGTCTTCATATG 1381 	දි දි	587 GTGGAACTTCAAGAAACATTTGGTTCAGCATTGCTGAGCAGGTATTTATGTGTTGAG 646
e - 5	දුරු පු	647 TCATGGCCATCTGATTCATACAGAATTGCCTTTACTACTTTATTGCTAGTTCAGTAT 706
lication No. US20030113798A1 ERAL INFORMATION: PLICANT: LifeSpan Biosciences PLICANT: Brown, Joseph P.	6 G	707 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGTCTGCAGAAGTATAAGCTGT 766
ANT: Burmer, Glenna C. MYT: Roush, Christine L. OF INVENTION: ANTIGENIC PEPTIDES EPERENCE: 1920-4-4	6 G	767 GGATTGTCCAACAAAGAAAACAGACTTGAAGAAAATGAGATGATGATCAACTTAACTCTTCAT 826
RRENT APPLICATION NUMBER: US/10/225,567A RRENT FILING DATE: 2001-12-19 LIOR APPLICATION NUMBER: 60/257,144 LIOR FILING DATE: 2000-12-19	oy.	827 CCATCCAAAAAGAGTGGCCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTATTCA 886
; NUMBER OF SEQ ID NOS: 2292 ; SCOTWARE Patentin version 3.1 ; SEQ ID NO 205 ; LENGTH: 445	ò 8	887 TTCATCAAAAAAACACAGAAGAAGAATATAGCAACAAGACAGCATGTGTTACCTGCTCCA 946
TYPE: PRT ORGANISM: Homo sapiens [0-225-567A-205	දි සි	947 GAAAGACCTTCTCAAGAACCACTCCAGAATACTTCCAGAAAACTTTGGCTCTGTAAGA 1006
Alignment Scores: 7.03e-218 Length: 445 Score: 2330.00 Matches: 445 Percent Similarity: 100.00% Conservative: 0	සු ද	1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGCTTTGAGATAAAA 1066
100.00% Mismatches: 93.95% Indels: 14 Gaps:	දි දි	1067 CCTGAAGAAAATTCAGATGTTCATGAATTGAGAGTAAAACGTTCTGTTACAAGAATAAAA 1126
US-09-771-956-4 (1-1406) x US-10-225-567A-205 (1-445) Qy	දි දි	1127 AAGAGATCTCGAAGTGTTTTCTACAGACTGACCATACTGATATTAGTATTTGCTGTTAGT 1186
1 MetaspleuGluleuaspGluTyrTyrAsnLysThrLeualaThrGluAsnAsnThrAla 20	8 8	TGGATGCCACTACACTTTTCCATGTGGTAACTGATTTTAATGACAATCTTATTTCAAAT 12
	a &	381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400 1247 AGGCATTTCAAGTTGGTGTATTGCATTTGTCATTTGGGGCATGATGTCCTGTTGTCTT 1306
167 CAGTATTTTCTGATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226	q q	ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 4
227 CTTATITTAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAACTTCCTCATA 286 61 LeulleLeumetalaLeumetLvsLvskyshashschlijvsThrThrVslaAsnPheLeulle 80	දුරු පු	AATCCATTCTATGGGTTTCTTAATAATGGGATTAAACCTGATTTAGLGTCCTTATA 13
GGCAATGTGGCCTTTTCTGAAATCTTGGTTGTTGTTTTTGCTCACCTTTCACACTGACG G1/A	දි දි	1367 CACTGTCTTCATATG 1381
347 TCTGTCTTGCTGGATCATGGCAAAGTCATGTGCCATATTATGCCTTTTCTT 406 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisTleMetProPheLeu 120	RESULT US-10-2 ; Seque: ; Publi	9 95-027-668 ace 668, Application US/10295027 cation No. US20030232350A1
407 CAATGTGTGTCTCTTTTGGTTTCAACTTTAATTTTAATATGCCATTGCCATTGTCAGGTAT 466	GENER APPL APPL APPL APPL APPL APPL APPL	, GENERAL INFORMATION: , APPLICANT: Afar, Daniel , APPLICANT: Aziz, Natasha , APPLICANT: Ginsberg, Wendy M. , APPLICANT: Gish, Kurt C.

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APPLICANT: Hevezi, Peter A.
APPLICANT: March, David H.
APPLICANT: March, David H.
APPLICANT: March, Chard
APPLICANT: March, Stan R.
APPLICANT: Wateon, Susan R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-9-15
PRIOR FILING DATE: 2000-11-13
PRIOR PLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PLING DATE: 2001-11-12
PRIOR PLING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR PLING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,214
PRIOR PLING DATE: 2001-12-14
PRIOR PLING DATE: 2002-11-10
PRIOR PLING DATE: 2002-11-10
PRIOR PLING DATE: 2002-11-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01
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Matches:
Conservative:
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1246 1006 1066 1126 1186 1306 340 420 360 400 280 946 300 160 586 180 646 200 706 220 994 240 826 260 886 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGTCTCCAGAAGTATAAGCTGT RESULT 10 US-10-181-906-14 Sequence 14, Application US/10181906 ; Publication No. US20040053864A1 CACTGTCTTCATATG 1381 |||||||||||||||| HisCysLeuHisMet 445 1187 1247 1307 1367 221 241 121 527 161 181 707 767 407 467 141 587 6 8 6 ઠે a d ò qq ò g b Sy 5 A B A g 8 8 à g & 셤 ò q Pb ò 쉱 Š 8 8 ઠે

Qy 707 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGTCTGCAGAAGTATAAGCTGT 766 Db 221 IleLeubroLeuValCysLeuThrValSerHisThrSerValCySARGSerTleSerCyS 240 Qy 767 GGATTGTCCAACAAGAAACAGACTTGAAGAAAATGAGATGATCAACTTTAACTCTTCAT 826 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260 Qy 827 CCATCCAAAAAGAGGGCCTCAGGTGAAACTCTCTGGCAGCATAATTGAAGTTATTCA 886 Db 261 ProSerLysLysSerGlyProGInValLysLeuSerGlySerHisLysFrpSerTyrSer 280 Qy 887 TTCATCAAAAAACAGAAGAAGATATAGCAACAAGACAGCATGTGTTACCTGCTCA 946 Db 281 PhelleLysLysHisArgArgArgArgArgArgArgArgArgArgArgArgArgA	1007 AGAGA CTCCTCTTCATCCAGTAAGTTCATACCAGGGGCCCCCACTTGCTTTGAGATAAAA 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 1067 CCTGAAGAAATTCAGATGTTCATGAATTGAGAGAGAAAAA	361 1187 381 1247		RESULT 11 US-09-771-956-9 ; Sequence 9, Application US/09771956 ; Sequence 9, Application US/09771956 ; GENERAL INFORMATION: ; APPLICANT: Bennett, Michele ; APPLICANT: Brodbeck, Robbin ; APPLICANT: Katuse, James ; TTHIR OF INVENTION: Chimeric Neuropeptide Y Receptors	1 Vo	; OTHER INFORMATION: Description of Artificial Sequence:YS/Y1 CHIMERA US-09-771-956-9 Alignment Scores: 1.77e-217 Length: 499 Score: 2326.00 Matches: 444
GENERAL INFORMATION: APPLICANT: Karsenty, Gerard APPLICANT: Aming, Michael APPLICANT: Aming, Michael APPLICANT: Aming, Michael APPLICANT: Ducy, Patricia TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA TITLE OF INVENTION: WODULATION OF NEUROPEPTIDE Y ACTIVITY FILE REFERENCE: 9142-020-999 CURRENT FILING DATE: 2002-11-13 PRIOR APPLICATION NUMBER: PCT/US01/02040 PRIOR FILING DATE: 2001-01-22 NUMBER OF SEQ ID NOS: 16 SOFTWARE: Patentin version 3.0 SEQ ID NO 14 LENGTH: 445 TYPE: PRT ORGANISM: Homo sapiens US-10-181-906-14	ignment Scores: od: No.: cd: No.: 2330.00 Matches: forest Similarity: forest Sim	Qy 47 ATGGATTTAGAGCTCGACGAGTATTATAACAAGACACTTGCCACAGAGAATAATACTGCT 106	Oy 167 CAGTATTTCTGATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226	81 GlyAenLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 347 TCTGTCTTGCTGGALGAGGATGTTTGGGGAAAGTCATGTGCCATATTATGCCTTTTCTT	Oy 467 CATATGATAAACATCCCATAICTAATAACTTAACAGCAACCATGGCTACTTTCTGGTA 526 141	Db 181 ValidudeudlaciumFPhediySerAlaLeudeuSerSerArgiyTHTHTT 200 Qy 647 TCATGGCCATCTGATTCATACAGAATTGCCTTTACTATCTTATTGCTAGTTCAGTAT 706

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Sequence 533, Application US/09826509

Publication No. US20030204073A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Libmann-Bruinsma, Karin
APPLICANT: Libm, I-Lin
APPLICANT: Libmann-Bruinsma, Karin
APPLICANT: Libmann-Bruinsma, Karin
APPLICANT: Libmann-Coupled Receptors
FILE REFERENCE: AREN-207
FILE REFERENCE: AREN-207
FILE REPERENCE: AREN-207
FRICH APPLICATION NUMBER: 60/195, 747
FRICH APPLICATION NUMBER: 09/170, 496
FRICH APPLICATION NUMBER: 09/170, 4 1277 CATTIGITGGGCATGATGTCCTGTTGTCTAATCCAATTCTATATGGGTTTCTTAATAAT 1336
421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProlleLeuTyrGlyPheLeuAsnAsn 440 1037 CCAGGGGTCCCCACTTGCTTTGAGATAAACCTGAAGAAAATTCAGATGTTCATGAATTG 1096 1097 AGAGTAAAAACGITCIGITACAAGAATAAAAAAGAGAICTCGAAGTGITTTCTACAGACTG 1156
161 AGVallysArgSerValThrargileLysSLgSerArgSerValPheTyrArgLeu 380 1157 ACCATACTGATATTAGTATTTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTGGTA 1216 341 ProGlyValProThrCysPheGlulleLysProGluGluAsnSerAspValHisGluLeu 360 106 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerSerLysPheIle 340 20 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: -771-956-4 (1-1406) x US-09-826-509-533 (1-445) 1337 GGGATTAAAGCTGATTTA 1354 ||||||||:: 441 GlylleGlnArgAspLeu 446 5.29e-217 2321.00 99.78% 99.78% 93.59% nt Similarity: Local Similarity: Match: T 12 -826-509-533 ment Scores:

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COURTIE: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/027,049
FILING DATE: 08-Apr-1996
CLASSIFICATION NUMBER: US/10/027,049
FILING DATE: 08-Apr-1996
CLASSIFICATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 36,149/WH 405
TELECOMMUNICATION NUMBER: 36,149/WH 405
TELECOMMUNICATION INPORMATION:
TELEFRANCE/DOCKET NUMBER: 36,149/WH 405
TELEFRANCE/DOCKET NUMBER: 36,1 g В 임 à 8 g ò $\dot{\delta}$ ð TCCIGITGICITAADCCAAITCTATATGGCTITCTTAATAATGGGAITAAAGCTGATTA 1354 TITGAGATAAAACCIGAAGAAAITICAGAIGITCAIGAAITGAGAGIAAAACGITCIGIT 1114 TTTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTGGTAACTGATTTTAATGACAAT 1234 CITATITICAAATAGGCATITICAAGTIGGIGIATIGCATITIGICATITIGTIGGGCATGAIG 1294 GGCTCTGTAAGAAGTCAGCTCTTCATCCAGTAAGTTCATACCAGGGGTCCCCACTTGC 1054 ACAAGAATAAAAAGAGATCTCGAAGTGTTTTCTACAGACTGACCATACTGATATTAGTA 1174 327 AlaSerValArgSerGlnLeuSerProSerSerLysVallleProGlyValProlleCys 346 LeulleSerAsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMet 426 874 934 307 227 754 814 TTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGAAATACTTCCAGAAAACTTT 994 634 694 514 TTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTCAGCATTGCTGAGCAGCAGGTAT AGTATAAGCTGTGGATTGTCCAACAAGAAACAGACTTGAAGAAAATGAGATGATCAAC TGGAGTIATICATICATCAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTG IleValArgTyrHisMetIleLysHisProlleSerAsnAsnLeuThrAlaAsnHisGly TTATGTGTTGAGTCATGGCCATCTGATTCATACAGAATTGCCTTTACTATCTCTTTATTG CTAGTICAGIAITATICIGCCCTIAGITIGICITACIGIAAGICATACAAGIGICIGCAGA TTAACTCTTCATCCATCCAAAAAGAGTGGGCCTCAGGTGAAACTCTCTGGCAGCCATAAA ATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAATTAACAGCAAACCATGGC TACTITCIGATAGCIACTGTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTG RESULT 14
US-10-027-049-4
ISEQUENCE 4, Application US/10027049
; Sequence 4, Application No. US20030022283A1
; Publication No. US20030022283A1
; GENERAL INFORMATION:
; APPLICANT: HU Ph.D., Yinghe
; McCaleb Ph.D., Michael L.
; Bloomquist Ph.D., Michael L.
; Flores-Riveros Ph.D., Jaime R. GIGICCCITATACACTGICTICATAIG 1381 248 995 (347 367 407 935 1055 1115 1175 1235 1295 427 1355 755 815 188 208 695 875 455 148 515 168 575 635 DP 셤 a 엄 셤 2 4 2 4 ò 염 장 8 6 8 S a S S B 임 8 S ò ò ò 8 ò ద 8 8 ò

and Nucleic

Cornfield Ph.D., Linda J. OF INVENTION: Neuropeptide Y Receptor

Seguences

SEQUENCES:

NUMBER OF

TITLE

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert of STREET: 32nd 1 STREET: 32nd 1 STREET: 12 COUNTY: USA ZIP: 60606 COMPUTER READABLE FORM:

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Mismatches:
Indels:
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Best Local Similarity: {
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                  Alignment Scores:
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                                                        AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
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CATATGATAAAACATCCCATATCTAATAATTTAACAGCAAACCATGGCTACTT
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Publication No. US20030022283A1
GENERAL INFORMATION:
APPLICANT: HP Ph.D., Yinghe
McCaleb Ph.D., Michael L.
Bloomquist Ph.D., Brian T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTGTCTTCATATG 1381
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Flores-Riveros Ph.D., Jaime R.
Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
Sequences
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/027,049
FILING DATE: 08-APP-1996
CLASSIFICATION: CURKNOWN
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3393
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert
STREET: 300 South Wacker Drive, 32nd
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
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2067.50
93.03%
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
DB:
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187 IGGAIGCCACTACACCTTTTCCAIGTGGTAACTGATTTTAATGACAATCTTATTTCAAAT 1246 CCTGAAGAAATTCAGATGTTCATGAATTGAGAGTAAAACGTTCTGTTACAAGAATAAAA 1126 947 GAAAGACCITCICAAGAACCACICCAGAATACTICCAGAAAACTTIGGCICTGTAAGA 1006 301 AlaGlyProSerGlnGlyLysHisLeuAlaVal---ProGluAsnProAlaSerValArg 319 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240 CATATGATAAAACATCCCATATCTAATAATTTAACACCAAACCATGGCTACTTTCTGATA 526 CCATCCAAAAAGAGIGGGCCTCAGGIGAAACICTCIGGCAGCCATAAAIGGAGITATICA 886 887 ITCATCAAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTTACCTGCTCCA 946 GCTACTGTCTGGACACTAGGTTTTGCCATCTGTTCTCCCCTTCCAGTGTTTCACAGTCTT 586 647 TCATGGCCATCTGATTCATACAGAATTGCCTTTACTATCTCTTTATTGCTAGTTCAGTAT 706 707 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGTCTGCAGAAGTATAAGCTGT 766 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140 HisCysLeuHisMet 444 1367 1067 1187 1307 467 141 527 827 Dp g g g OY Db g & 8 B 8 8 8 8 6666 9 9 S 8 ò 8 8 8 ò ò Ś

Search completed: October 21, 2004, 12:07:40 Job time : 209 secs

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